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94043 (US). RANK, David, R. [US/US]; 117 El Dorado  
Commons, Fremont, CA 94539 (US).

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(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharma-  
cia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ  
08855 (US).

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(71) Applicant (*for all designated States except US*): MOLEC-  
ULAR DYNAMICS, INC. [—/US]; 928 East Arques Av-  
enue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PENN, Sharron,  
G. [GB/US]; 617 South Delaware Street, San Mateo, CA  
94402 (US). HANZEL, David, K. [US/US]; 988 Loma  
Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wen-  
sheng [CN/US]; 210 Easy Street #25, Mountain View, CA

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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE  
EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene  
expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the  
brain and their use in methods for detecting gene expression.

WO 01/57275 A2

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.  
patent application serial nos. 09/632,366, filed August 3,  
2000 and 09/608,408, filed June 30, 2000; claims the  
benefit under 35 U.S.C. s 119(e) of U.S.provisional patent  
10 application serial nos. 60/236,359, filed September 27,  
2000, 60/234,687, filed September 21, 2000, 60/207,456,  
filed May 26, 2000, and 60/180,312, filed February 4, 2000;  
and further claims the benefit under 35 U.S.C. s 119(a) of  
UK patent application no. 0024263.6, filed October 4, 2000,  
15 the disclosures of which are incorporated herein by  
reference in their entirety.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

20

The present application includes a Sequence Listing in  
electronic format, filed pursuant to PCT Administrative  
Instructions 801 - 806 on a single CD-R disc, in  
triplicate, containing a file named pto\_BRAIN.txt, created  
25 24 January 2001, having 25,840,972 bytes. The Sequence  
Listing contained in said file on said disc is incorporated  
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived  
single exon microarrays useful for verifying the expression  
of regions of genomic DNA predicted to encode protein. In  
particular, the present invention relates to unique genome-  
35 derived single exon nucleic acid probes expressed in human

brain and single exon nucleic acid microarrays that include such probes.

#### Background of the Invention

5           For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

          For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

          More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

          One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,  
*Science* 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches – and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species – there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of  
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,  
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the  
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many  
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that  
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting  
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et  
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex  
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

          Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that  
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.  
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

### 30 Summary of the Invention

          The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional  
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel  
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids  
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single  
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably  
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality  
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000  
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a  
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,  
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least  
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is  
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane  
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,  
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring  
5 human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high  
10 stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the  
15 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon  
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,  
25 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent  
35 labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon  
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency..

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,  
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in  
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types  
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ  
35 ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for  
10 electronic search, query, and analysis of such annotated sequence.

### Detailed Description of the Invention

#### Definitions

15 As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each  
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called  
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books  
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary  
35 planar substrate, as is described, *inter alia*, in Brenner

*et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5           As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick  
10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

          As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid  
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the  
20 requirement that the probe hybridize to mRNA.

          As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence  
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

          As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing  
30 the predicted exon.

          As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a  
35 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

#### Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence  
5 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A  
10 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

15 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can  
20 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part  
25 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100  
30 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the  
35 National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic  
5 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by  
10 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into  
15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into  
20 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will  
25 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental  
30 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the  
35 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the  
5 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously  
10 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily  
15 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other  
20 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity  
25 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10)  
30 ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query  
35 criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable  
5 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,  
10 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and  
15 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual  
20 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,  
25 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known  
30 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be  
35 removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired  
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower  
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest  
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,  
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as  
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting  
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating  
35 transcription, regulating message transport after

transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability  
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function  
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as  
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for  
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)  
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene  
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;  
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison  
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the  
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process  
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to  
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon  
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene  
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible  
35 secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving

5 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such

10 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process

15 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in

20 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the

25 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression

30 of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon

35 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the  
5 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with  
10 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

15 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer  
20 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify  
25 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

30 Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it  
35 has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5           The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic  
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased  
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves  
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later  
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least  
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for  
35 amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, 5 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 10 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

15 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 20 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 25 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

30 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 35 readily be used. As further described in Example 1, 16 or

32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create  
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.  
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using  
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on  
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.  
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads  
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high  
35 throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will  
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one  
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created  
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or  
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific"  
30 libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure  
35 expression only of those genes found in EST libraries,

shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective  
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be  
10 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the  
15 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA  
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present  
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse  
35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,  
5 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric  
10 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-  
15 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present  
20 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the  
25 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically  
30 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector  
35 sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly  
5 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through  
10 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-  
15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker  
20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include  
25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to  
30 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without  
35 such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such  
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present  
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual  
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be  
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often  
25 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized  
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic  
5 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to  
10 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the  
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present  
20 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved  
25 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention  
30 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their  
35 complementary target sequence, and thus causes large

percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which  
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization  
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the  
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can  
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see  
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of  
35 nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As  
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are  
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain  
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for  
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived  
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate  
35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits  
5 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-  
10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'  
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

20 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

25 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered  
30 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing  
35 information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate  
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a  
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental  
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be  
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide  
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local  
35 alignment search tool"). The results of such query -

including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to  
5 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data  
10 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or  
15 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or  
20 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence  
25 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic  
30 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given  
35 the number of nucleotides typically represented in an

annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention  
5     herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10             As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides  
15     can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other  
20     pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.  
25     Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or  
30     fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity  
35     or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection  
5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional  
10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

15 Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method  
20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c  
30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.  
35 For example, rectangles 83a can represent the results from

GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links  
5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be  
10 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical  
15 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of  
20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of  
25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to  
30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to  
35 indicate expression intensity. As discussed *infra*, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

#### Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of  
5 the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon  
15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these  
20 ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in  
25 brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness  
30 of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades  
35 Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5           Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence  
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2  
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

          Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic  
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and  
25 internal neurofibrillary tangles.

          Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

30           At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding  
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing  
5 (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological  
15 transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed  
20 optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple  
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general population, but could discern no definite genetic pattern  
30 of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet.  
7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to  
35 the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2  
different sites, as have sites on the X chromosome. Wei et  
al., Nature Genet. 25:376-377 (2000) report more  
specifically that the NOTCH4 locus is associated with  
5 susceptibility to schizophrenia.

In general, however, it is believed that  
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.  
8:1729-1739 (1999) undertook a systematic search for  
10 linkage in 196 affected sib pairs (ASPs) with  
schizophrenia. Using 229 microsatellite markers at an  
average intermarker distance of 17.26 cM, followed in a  
second stage by a further 54 markers allowing the regions  
identified in stage 1 to be typed at an average spacing of  
15 5.15 cM, Williams et al. considered results on chromosomes  
4p, 18q, and Xcen as suggestive; however, given the scores,  
Williams et al. interpreted their results as suggesting  
that common genes of major effect (susceptibility ratio  
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.  
81(5):364-76 (1998), in a genome-wide search for  
schizophrenia susceptibility genes, found that twelve  
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and  
22) had at least one region with a nominal P value <0.05,  
25 that two of these chromosomes had a nominal P value <0.01  
(chromosomes 13 and 16), and that five chromosomes (1, 2,  
4, 11, and 13) had at least one marker with a lod score  
>2.0, suggesting the existence of multiple loci that  
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are  
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,  
paroxysmal disorders of cerebral function (seizures); that  
is, by sudden, brief attacks of altered consciousness,  
35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically  
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy  
bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion  
diseases (Creutzfeld-Jakob, Gerstmann-Straussler-Senker,  
10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral  
degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-  
telangiectasia, amyotrophic lateral sclerosis, bulbospinal  
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid,  
mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy,  
Pelizaeus-Merzbacher disease, Canavan disease,  
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis,  
paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal  
degeneration, stiff-man syndrome and Von Hippel-Lindau  
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma,  
fibrillary astrocytoma, pilocytic astrocytoma,  
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma,  
primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous  
35 system that likely have genetic components include the

various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10           The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20           For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are be obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5           Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10           The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15           Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20           Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);  
35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine  
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,  
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and  
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the  
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,  
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway  
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047;  
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a  
form and quantity suitable for amplification, where the  
5 amplified product is thereafter to be used in the  
hybridization reactions that probe gene expression.  
Typically, such probes are provided in a form and quantity  
suitable for amplification by PCR or by other well known  
amplification technique. One such technique additional to  
10 PCR is rolling circle amplification, as is described, *inter*  
*alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and  
international patent publications WO 97/19193 and  
WO 00/15779. As is well understood, where the probes are  
to be provided in a form suitable for amplification, the  
15 range of nucleic acid analogues and/or internucleotide  
linkages will be constrained by the requirements and nature  
of the amplification enzyme.

Where the probe is to be provided in form  
suitable for amplification, the quantity need not be  
20 sufficient for direct hybridization for gene expression  
analysis, and need be sufficient only to function as an  
amplification template, typically at least about 1, 10 or  
100 pg or more.

Each discrete amplifiable probe can also be  
25 packaged with amplification primers, either in a single  
composition that comprises probe template and primers, or  
in a kit that comprises such primers separately packaged  
therefrom. As earlier mentioned, the ORF-specific  
5' primers used for genomic amplification can have a first  
30 common sequence added thereto, and the ORF-specific 3'  
primers used for genomic amplification can have a second,  
different, common sequence added thereto, thus permitting,  
in this embodiment, the use of a single set of 5' and 3'  
primers to amplify any one of the probes. The probe  
35 composition and/or kit can also include buffers, enzyme,

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 – 25,434, respectively, for probe SEQ ID NOS. 1 – 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

5           Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a  
10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization  
15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room  
20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single  
25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more  
30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more  
35 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in

Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term  
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.  
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the  
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray  
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a  
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means  
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon  
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 -  
5 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as  
10 protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New  
15 England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Emoc Solid Phase Peptide  
20 Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles  
25 of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino  
30 acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a  
35 further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

10

#### Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding  
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a  
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

#### 15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes  
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,  
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3  
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit  
35 subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant  
5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of  
15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest  
20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range  
25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region,  
30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process  
35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

5                    Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and  
10                    standard protocols.

                  Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some  
15                    submitted sequence data.

                  Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression  
20                    ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not  
25                    shown).

                  The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII  
30                    Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

35                    Each of the probe sequences was BLASTed against

the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \times 10^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \times 10^{-5}$  to  $1 \times 10^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

## EXAMPLE 2

### Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

100 $\mu$ M dATP, 100  $\mu$ M dGTP, 100  $\mu$ M dTTP, 50  $\mu$ M dCTP, 50  $\mu$ M  
Cy3-dCTP or Cy5-dCTP 50  $\mu$ M, and 200 U Superscript II  
enzyme. The reaction was incubated for 2 hours at 42°C.  
After 2 hours, the first strand cDNA was isolated by adding  
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.  
The reaction was then purified using a Qiagen PCR cleanup  
column, increasing the number of ethanol washes to 5.  
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured  
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA  
corresponding to 50 pmoles of each dye were then dried in a  
Speedvac, resuspended in 30  $\mu$ l hybridization solution  
containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  
 $\mu$ g/ $\mu$ l human c<sub>ot</sub>1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a  
coverslip, with the array placed in a humid oven at 42°C  
overnight. Before scanning, slides were washed in 1X SSC,  
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%  
SDS, at 55°C for 20 minutes. Slides were briefly dipped in  
20 water and dried thoroughly under a gentle stream of  
nitrogen.

Slides were scanned using a Molecular Dynamics  
Gen3 scanner, as described. Schena (ed.), Microarray  
Biochip: Tools and Technology, Eaton Publishing  
25 Company/BioTechniques Books Division (2000) (ISBN:  
1881299376).

Although the use of pooled cDNA as a reference  
permitted the survey of a large number of tissues, it  
attenuates the measurement of relative gene expression,  
30 since every highly expressed gene in the tissue/cell type-  
specific fluorescence channel will be present to a level of  
at least 10% in the control channel. Because of this fact,  
both signal and expression ratios (the latter hereinafter,  
"expression" or "relative expression") for each probe were  
35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray  
5 experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

10 Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as  
15 measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay  
20 methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the  
25 power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides  
30 correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very  
35 low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray  
 5 hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
 10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
 15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed  
 20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless  
 25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2  
were similar to actin (AL035701-2; AL034402-1), and 6 were  
found to be homologous to glyceraldehyde-3-phosphate  
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,  
5 AC006064-K; AC035604-3; AC006064-L). These genes are often  
used as controls or housekeeping genes in microarray  
experiments of all types.

Other interesting genes highly expressed in brain  
were a ferritin heavy chain protein, which is reported in  
10 the literature to be found in brain and liver (Joshi et  
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result  
duplicated with the array. Other highly expressed chip  
sequences included a translation elongation factor 1 $\alpha$   
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-  
15 chromosome RNA-binding motif (Chai et al., *Genomics*  
49(2):283-89 (1998)) (AC007320-3). A low homology analog  
(AP00123-1/2) to a gene, DSCR1, thought to be involved in  
trisomy 21 (Down's syndrome), showed high expression in  
both brain and heart, in agreement with the literature  
20 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we  
selected the BAC AC006064 to be included on the array.  
This BAC was known to contain the GAPDH gene, and thus  
could be used as a control for the ORF selection process.  
25 The gene finding and exon selection algorithms resulted in  
choosing 25 exons from BAC AC006064 for spotting onto the  
array, of which four were drawn from the GAPDH gene. Table  
3 shows the comparison of the average expression ratio for  
the 4 exons from BAC006064 compared with the average  
30 expression ratio for 5 different dilutions of a  
commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$
Lung	-4.95 $\pm$ 0.93	-3.75 $\pm$ 0.21
Placenta	-3.56 $\pm$ 0.25	-3.52 $\pm$ 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments."

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

20

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they  
5 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):  
red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
10 turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,  
20 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe  
25 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-  
30 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented  
35 fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOs.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified  
5 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.  
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because  
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the  
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were  
35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

#### EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of  
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.
16. A single exon nucleic acid probe as claimed in any one.  
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
17. A single exon nucleic acid probe as claimed in any one  
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.  
25
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
21. A single exon nucleic acid probe as claimed in any one  
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

5       contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then measuring the label detectably bound to each probe of  
10       said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15       algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the brain of said eukaryote, said probe is a  
20       single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

30       identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,  
35       wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID  
5 NOS: 1 - 25,434 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of  
SEQ ID Nos: 1 - 25,434.

10 27. A peptide comprising a sequence as set out in any of  
SEQ ID NOS: 25,435 - 37,811.

Page 1 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	25868	6.47				
869	13638	26308	15.92				
1022	13782		2.16				
1279	14029	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1609	14355	27044	3.19				
1633	14379	27068	6.1				
1718	14461	27160	3.31				
1743	14485	27184	1.44				
1750	14492	27192	6.78				
1884	14621	27331	1.44				
1971	14707	27426	2.14				
2162	14892	27627	2.7				
2277	15003	27743	2.91				
2578	15292	28028	1				
2578	15292	28028	1				
3181	16944	28596	2.83				
3442	16198	28948	1.42				
3505	16261	28915	12.04				
3549	16304		1				
3649	16402	29042	1.67				
3928	16678		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29613	0.97				
4248	16989	29614	0.97				
4303	17042		1.07				
4361	17099	29734	0.76				
4784	17516	30138	0.99				
4983	17706	30310	5.38				
4995	17718	30323	1.3				
5176	17985	30500	1.57				
5176	17985	30501	1.67				

Page 2 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5338	18138		4.3				
5510	18308		6.14				
5593	18138		3.97				
5848	18443	31359	0.8				
5884	18449	31302	3.28				
5932	25082	31673	1.62				
5958	18740	31699	1.76				
6322	18082		1.27				
6454	19222	32220	1.1				
6454	19222	32221	1.1				
7028	19717	32774	1				
7029	19717	32776	1				
7311	18994	33071	1.78				
7311	18994	33072	1.76				
7712	20378		0.61				
7860	20655	33780	1.4				
8384	21077	34214	1.49				
8759	21451	34598	0.59				
8759	21451	34599	0.59				
9434	22112	35287	2.67				
9666	22318	35515	0.77				
9782	22433	35638	1.24				
9922	22570	35787	0.94				
10328	22975	36194	0.62				
10328	22975	36195	0.62				
10582	23277		2.53				
10749	25131	36879	1.34				
10852	23629		2.2				
11030	23701	36968	1.84				
11332	24023	37328	2.02				
11485	24088		2.47				
12313	24735		1.52				
12809	24916	31006	2.36				
5951	18743	31703	17.79	9.8E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18

Page 3 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7005	20600	33730	1.74	9.8E+00	U32716.1	NT	Haemophilus Influenzae Rd section 31 of 163 of the complete genome
8043	22285	35489	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
8043	22295	35490	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
6901	19839	32684	0.73	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
6901	19839	32685	0.73	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22968	36187	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10321	22968	36188	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2671	15381	28119	1	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polypeptide mRNA, partial cds
2671	15381	28120	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polypeptide mRNA, partial cds
2624	16690	28334	2.87	9.4E+00	A9043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
7997	20892	33820	0.91	9.3E+00	AF100980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8001	21592	34733	3.08	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.46	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5214	18022	30646	2.46	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
8330	21997		0.83	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6945	18727	31685	5.55	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6287	19060	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
6287	19060	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
430	13216	25881	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
8365	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11122	23791		2	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8051	20745		0.89	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	19931		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8259	20953	34090	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5711	18504	31426	2.66	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5'
8651	21343	34487	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Page 4 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15743	28390	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6931	18667	32713	0.71	7.2E+00	BE179080.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22161		8.63	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P05860	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
8882	22632	36729	3.37	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
8181	20875	34011	1.92	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scars melanocyte 2NbmH Homo sapiens cDNA clone IMAGE:291860 5'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
9031	21721		1.29	6.8E+00	P36307	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
10108	22757	35969	3.24	6.8E+00	Q03570	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
5202	18010		0.72	6.6E+00	Q96028	SWISSPROT	602162573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
6450	19218	32216	0.61	6.6E+00	BF672121.1	EST_HUMAN	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8974	22622	35827	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8974	22622	35828	2.36	6.6E+00	Q9ZE07	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
11073	23743		1.97	6.6E+00	Q10309	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
9079	21768	34931	7	6.5E+00	P03374	SWISSPROT	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
10203	22861	36067	0.49	6.5E+00	BE868001.1	EST_HUMAN	Schizaphyllum commune unknown mRNA
9842	22284	35488	1.55	6.2E+00	AY010901.1	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
10480	23106	36337	0.5	6.2E+00	6754621	NT	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
6938	19871	32717	1.48	6.0E+00	BE780163.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (617)
9718	22367	35595	0.46	6.0E+00	AP000006.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36274	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36275	0.67	6.0E+00	AE001862.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6428	19186	32183	7.32	5.9E+00	AF155142.1	NT	Homo sapiens DESC1 protein (DESC1), mRNA
3514	18270		0.99	5.8E+00	7681557	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7061	19752	32816	0.95	5.7E+00	AF302046.1	NT	

Page 5 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7061	19752	32817	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11458	23223	36468	2.59	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
6157	18934	31801	0.89	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10878	23369		1.28	5.5E+00	AF175426.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11454	23221	36455	3.09	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
6830	19492	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
6830	19492	32516	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
7769	20465		1.54	5.4E+00	Q91082	SWISSPROT	
8698	21390	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8698	21390	34535	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8936	22884	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
8936	22884	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17468	30102	1.32	6.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
7878	20873		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8882	21573		0.49	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11828	24225	37548	3.2	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
6377	18177		0.91	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-188-608 HT0691 Homo sapiens cDNA
10271	22919		0.95	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retroltransposable element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8861	21652	34698	0.9	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
8725	22376	35577	1.19	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6183	18969	31944	0.72	6.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.59	5.0E+00	BF308581.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22877	36197	3.07	5.0E+00	AF102445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11260	23922	37214	8.95	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10132	22780		0.71	4.8E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4039	16784		10.88	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8054	20748	33879	0.47	4.8E+00	BF397809.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8439	21131		6.28	4.8E+00	AW750087.1	EST_HUMAN	PM0-BT0547-310100-002-804 BT0547 Homo sapiens cDNA
283	13090	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098718 5'

Page 6 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
284	13090	25731	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3268	16030	28679	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9095	21763	34948	1.18	4.6E+00	BE649437.1	EST_HUMAN	7686g10.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ;contains element PTR5 repetitive element ;
9095	21763	34949	1.18	4.6E+00	BE649437.1	EST_HUMAN	7686g10.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ;contains element PTR5 repetitive element ;
10287	22835		0.61	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11054	23724		2.31	4.6E+00	D63999.1	NT	Synechocystis sp. PCC6803 complete genome, 18/27, 2287260-2392728
11605	24204	37528	2.59	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11762	24353	37685	1.78	4.5E+00	BF66841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3035	15801	28447	0.98	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3035	15801	28448	0.98	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
6109	18866		1.68	4.4E+00	X13414.1	NT	Murine 1 gene for MHC class II(a) associated invariant chain
6027	18807		0.68	4.3E+00	AF056879.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7338	20019	33097	2.03	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
7615	20186	33280	0.65	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
10769	23453	36696	7.64	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5507	18305	31206	0.87	4.2E+00	P51828	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6874	18691	32827	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6874	19591	32628	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8659	21650	34697	4.68	4.2E+00	AB09013.1	EST_HUMAN	w67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
8818	22469	36672	1.06	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10049	22697		0.46	4.2E+00	P40866	SWISSPROT	HEXOSE TRANSPORTER HXT8
5846	25079	31569	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
5846	25079	31570	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7012	19704	32760	0.84	4.1E+00	BE256668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7111	19798	32863	0.65	4.1E+00	BF247839.1	EST_HUMAN	60185930F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068758 5'
7659	20229	33332	8.73	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7681	20345		0.62	4.1E+00	AB041523.1	NT	Palinopecten yessoensis mRNA for calcineurin A, complete cds
7683	20347	33459	4.32	4.1E+00	P28954	SWISSPROT	GENE 68 PROTEIN

Page 7 of 536  
Table 4

Single Exon Probes Expressed in Brain

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7693	20347	33460	4.32	4.1E+00	P28994	SWISSPROT	GENE 68 PROTEIN
7817	20512	33638	2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive sdo LTR element in the RNU2 locus
9440	22118	35295	0.67	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.48	4.1E+00	BF692425.1	EST_HUMAN	602247638F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10205	22853		0.48	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10800	23493		3.06	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
10892	23572		11.69	4.1E+00	BE883880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809051 5'
3633	16289		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	19500	32524	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5372	19500	32525	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32524	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32525	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7089	19778	32843	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21484	34611	0.45	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
9843	22494	35695	0.44	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10085	22713	35931	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14549	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11637	24137	37444	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3494	16290	28904	4.61	3.9E+00	X64518.1	NT	N. labacum chitinase gene 50 for class I chitinase C
4287	17026		8.24	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5572	18369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5572	18369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6591	19354	32367	0.55	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6774	19518	32546	4.62	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION

Page 8 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	18946	33022	4.3	3.9E+00	M2907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8216	20910	34046	1.86	3.9E+00	X55865.1	NT	X. laevis mRNA for M4 muscarinic receptor
11365	23178	36403	3.3	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2636	15347		0.9	3.8E+00	AE001582.1	NT	Helicobacter pylori, strain J99, section 123 of 132 of the complete genome
6257	19070	32054	0.96	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
6873	19590	32626	0.66	3.8E+00	AI493849.1	EST_HUMAN	q25107.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34161	1.1	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9694	22346		0.62	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884
4001	16748	29379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7066	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8609	21301		0.55	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GOK), nuclear gene encoding mitochondrial protein, mRNA
9076	21765	34928	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24057	37363	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24057	37364	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
578	13359	25986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4745	17477		1.06	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17993	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131018 5'
8450	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone t608
8450	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone t608
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
10759	23444		4.07	3.6E+00	M99795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3241	16003	28652	1.1	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
5911	18695		1.17	3.5E+00	L42898.1	NT	Yg40c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6118	18896	31864	1.18	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8383	21076		0.56	3.5E+00	P24557	SWISSPROT	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8930	21621	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8930	21621	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	contains Alu repetitive element; contains element MSR1 repetitive element;
9393	22055	35227	0.86	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

Page 9 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10417	23083	36283	0.48	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	26933	2.94	3.4E+00	AF264577.1	NT	Bressica napus RPB5d mRNA, complete cds
7261	18945	33021	2.64	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7601	20267	33374	0.69	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8577	21289		0.7	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROMK1, ROMK2, ROMK3, ROMK4, ROMK5, and ROMK6 (KCNJ1) gene, complete cds
8972	21662	34813	0.67	3.4E+00	AJ229042.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
6010	21700	34850	0.54	3.4E+00	AJ250587.1	NT	Homo sapiens partial MSS1 gene, complete cds
10164	22812	36030	2.97	3.4E+00	AF013187.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11619	24119	37429	1.89	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5977	18769	31722	1.57	3.3E+00	Q08689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5977	18759	31723	1.57	3.3E+00	Q08689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7794	20489	33611	0.79	3.3E+00	AF111189.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
488	13273	25908	1.64	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4004	13273	25908	0.9	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4879	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5481	18280	31176	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5481	18280	31177	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18988	31964	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6214	18988	31965	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7605	20176	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8928	21619	35283	4.51	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9430	22108	35283	0.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
10041	22889	35907	2.03	3.2E+00	AB016081.2	NT	Oryza latipes OIGC8 gene for guanylyl cyclase C, complete cds
11946	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.46	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C3E2.02 IN CHROMOSOME 1
7287	18970	33047	0.93	3.1E+00	P62178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (C1PT)

Table 4  
Single Exon Probes Expressed In Brain

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7627	20263		0.94	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
7988	20861	33807	0.48	3.1E+00	P40885	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8500	21192	34333	4.36	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8500	21192	34334	4.38	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9168	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9798	22447	35652	0.59	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
9888	22538		0.63	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10234	22882	36095	5.52	3.1E+00	P49385	SWISSPROT	DEOXYHYPERUSINE SYNTHASE (DHS)
11440	23207		2.66	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
11463	24066		3.28	3.1E+00	S56680.1	NT	retinotic acid nuclear receptor isoform beta 2 [mlca, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
2842	15810	28289	1.09	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
6254	18060	30699	1.32	3.0E+00	X63096.1	NT	S.aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6481	19228	32228	0.83	3.0E+00	X66037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6481	19228	32229	0.83	3.0E+00	X66037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7055	19746		9.09	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (SCH61)
7096	19765		0.8	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8805	21497		1.2	3.0E+00	X67838.1	NT	B.napus DNA for myrosinase
10192	22840	36055	0.62	3.0E+00	Q56905	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10944	23240	36474	1.57	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10931	23611	36860	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10931	23611	36861	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11578	24177	37492	2.72	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2004	14740	27464	2.28	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
6809	19470	32493	1.74	2.8E+00	Z36879.1	NT	F.pfringel gdsrA gene for P-protein of the glycine cleavage system
7110	19768	32881	5.21	2.8E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

Page 11 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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7110	19798	32882	5.21	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	6.84	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7958	20691	33819	1.03	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4163059 6'
1440	14187	28872	4.4	2.8E+00	AF186398.1	NT	Buxus harlandii malurase K (malK) gene, partial cds; chloroplast gene for chloroplast product
1629	14375		2.74	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32968	6.72	2.8E+00	8393724	NT	Mus musculus endonuclease (LOC53423), mRNA
9513	22168		0.54	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3684807 5'
10588	19892	32968	1.32	2.8E+00	8393724	NT	Mus musculus endonuclease (LOC53423), mRNA
224	13036	25872	13.51	2.7E+00	6879306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
224	13036	25873	13.51	2.7E+00	6879306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
6484	18263	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8045	20739		0.6	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8867	21558		1.83	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8332	20403	33519	0.73	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb.M17733
10387	23043		1.75	2.7E+00	BE083527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4628	17361	29894	6.15	2.6E+00	AF088749.1	NT	CM0-BT0281-031195-087-104 BT0281 Homo sapiens cDNA
6460	18259	31149	1.68	2.6E+00	6766601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
6460	18259	31150	1.68	2.6E+00	6766601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5736	18528		0.59	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	26424		0.82	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7600	20266		6.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7958	20553	33778	1.13	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 18 through 27, and complete cds
7958	20553	33777	1.13	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
8957	22210	35395	2.83	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10263	22901		1.67	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10953	23630	36878	1.32	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12660	26304		3.17	2.6E+00	11419220	NT	Hantaavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14195	26878	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
							Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Page 12 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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1448	14195	26979	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31435	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6630	19392	32406	0.64	2.5E+00	D30082.1	NT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7659	20323	33431	0.99	2.5E+00	AW049158.1	EST_HUMAN	QV4-F70005-110500-205-g07 FT0005 Homo sapiens cDNA
7700	20363	33477	0.68	2.5E+00	4502802	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9001	21691	34841	1.53	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9752	22403	35608	0.67	2.5E+00	BE297758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
11943	24498		3.08	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3012	15778	28428	1.13	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4849	17578	30203	6.09	2.4E+00	4503352	NT	Homo sapiens double G2-like domains, alpha (DGC2A) mRNA
5920	18705	31657	4.18	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7280	19984	33040	0.78	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	19984	33041	0.78	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8039	20734	33865	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8039	20734	33866	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8110	20804		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8549	21241		1.61	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031288-011-405 PT0004 Homo sapiens cDNA
8727	21419	34563	7.36	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9938	22586	35788	2.68	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9938	22586	35788	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10007	22655	35868	1.86	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10143	22791		6.65	2.4E+00	P06089	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10220	22808	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	tr63f08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22808	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	tr63f08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10490	23136	36384	0.87	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIFQ
11331	24022	37327	2.16	2.4E+00	AF158652.2	NT	Frageria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1231	13980	26660	13.6	2.3E+00	Z48724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4102	18845		1.35	2.3E+00	AJ401081.1	NT	Bos taurus partial cyb gene for cytochrome b

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5744	18538		0.95	2.3E+00	N86245.1	EST_HUMAN	J73407 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYL CARBOXYPEPTIDASE
7354	20035	33113	2.47	2.3E+00	6978564	NT	Rattus norvegicus ATPase, Cax+ transporting, ubiquitous (Atp2a3), mRNA
7495	25425		3.07	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	1.01	2.3E+00	X60265.1	NT	M.mazaei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
8008	21698	34846	0.64	2.3E+00	5835317	NT	Polyturus ornatinipinnis mitochondrion, complete genome
8088	21767	34919	1.8	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10704	23395	36632	3.83	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11782	24373	37703	3.03	2.3E+00	BF5641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11782	24373	37704	3.03	2.3E+00	BF5641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24842	31099	6.84	2.3E+00	BE995237.1	EST_HUMAN	601433873F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
3998	16746	29378	0.85	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4278	17017	29844	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4278	17017	29845	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
6258	18064	30692	12.73	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)<>
5258	18064	30693	12.73	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)<>
5763	18594	31478	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5763	18594	31479	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5971	18753	31714	9.84	2.2E+00	BE260383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6281	18035	32010	3.87	2.2E+00	Q00395	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6502	19267	32269	3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6861	17698		3.84	2.2E+00	AA684674.1	EST_HUMAN	U95802 st NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7217	19802	32975	0.9	2.2E+00	AA137027.1	EST_HUMAN	zp97704.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7507	20178	33272	19.2	2.2E+00	AA449012.1	EST_HUMAN	zx05910.1 Sceres total fetus NB2HF8 9w Homo sapiens cDNA clone IMAGE:785634 5'
7589	20257	33366	0.72	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8001	20696	33823	0.58	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.xt NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);

Page 14 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8001	20696	33824	0.58	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8241	21920		11.02	2.2E+00	BE741678.1	EST_HUMAN	001594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948661 5'
8468	25124		2.28	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
8953	22601	35804	1.1	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares, placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1893865 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
8953	22601	35805	1.1	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares, placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1893865 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
8998	22844	35858	2.68	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4078391 5'
10393	23000	36217	3.11	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11418	23185	36415	3.47	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11616	24214	37639	5.89	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
556	16345	25967	8.3	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3675	16330		1.08	2.1E+00	AW449368.1	EST_HUMAN	UIH-B13-ekd-e-08-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6041	18821		0.89	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6710	18825	32689	3.95	2.1E+00	Q70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6946	19428	32443	6.72	2.1E+00	N29575.1	EST_HUMAN	y08a10.s1 Soares, melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
8395	21088		1.97	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1312	14060	26735	0.97	2.0E+00	AF204827.1	NT	Oryctolagus cuniculus Nat K+-ATPase beta 1 subunit mRNA, complete cds
1869	14318		2.61	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2145	14875	27609	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2145	14875	27610	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4080	18824	28450	2.2	2.0E+00	AW664498.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4080	18824	28451	2.2	2.0E+00	AW664498.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7449	20125		0.92	2.0E+00	P07568	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7923	20618	33745	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7923	20618	33746	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8820	21512	34658	3.15	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12481	26285	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.8E+00	6754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (lpr1), mRNA
5511	18309	31210	4.77	1.8E+00	6754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (lpr1), mRNA
6008	18790	31753	1.32	1.9E+00	BE66955.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6556	19321		0.75	1.9E+00	AW845889.1	EST_HUMAN	MRO-CT0063-071089-002-g02 CT0063 Homo sapiens cDNA
6850	18412		2.46	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34180	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21249		2.94	1.9E+00	BF380206.1	EST_HUMAN	CM3-MT0114-010800-323-h12 MT0114 Homo sapiens cDNA
8782	21484		1.33	1.8E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9530	22183	35387	0.59	1.9E+00	AA669125.1	EST_HUMAN	ab94804.61 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element contains element L1 L1 repetitive element ;
10482	23108	36339	0.62	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3088	15854	28488	1.3	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3118	15883	28522	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3118	15883	28523	1.67	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5777	18588		1.91	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6013	18784	31757	1.32	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4127364 5'
6305	19077		1.12	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6641	19403	32418	1.64	1.8E+00	BF305852.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
6958	19440	32455	1.79	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8368	21061	34201	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34202	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8763	21445	34593	1.98	1.8E+00	O49281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9073	21782	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	yh72c08.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:135278 5'
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA

Page 16 of 536  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9749	22400	35606	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10452	23098		0.63	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12276	25236		5.29	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
1086	13844	28502	2.21	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27734	2.29	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2372	16094	27833	2.56	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878137 3'
4428	17162	29782	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31223	1.77	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5927	18711	31666	3.28	1.7E+00	Q911TR	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7118	19806	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19806	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7763	20449	33573	0.91	1.7E+00	AF021336.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7832	20627	33755	1.13	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
7981	20656	33781	0.59	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCL CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4214669 5'
8440	21132	34268	0.6	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8605	21297	34440	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8605	21297	34441	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9047	25123	34892	2.18	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9506	22169		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10071	22719		0.48	1.7E+00	AW953681.1	EST_HUMAN	EST365761 MAGE resequences, MAGC Homo sapiens cDNA
11596	24195	37514	2.57	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
12231	24684	31074	1.9	1.7E+00	AI674443.1	EST_HUMAN	tu82407.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1
12717	24990	30970	1.84	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element ;
2027	14762	27491	18.51	1.6E+00	AF199339.1	NT	qf50p01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1 repetitive element ;
							Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2036	14771	27500	3.75	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2282	15007		1.24	1.6E+00	X88373.1	NT	B. napus gene encoding endo-polygalacturonase
2861	15727	28377	1.61	1.6E+00	W59426.1	EST_HUMAN	z425f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
4011	16757		5.68	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310581 3'
4319	17058	28682	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA6) mRNA, complete cds
4319	17058	28683	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17669	30278	0.84	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.88	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5737	18529	31450	2.16	1.6E+00	L04908.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
5823	18612	31543	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6610	19373	32387	1.08	1.6E+00	AW284881.1	EST_HUMAN	UIH-B12-ahr-b-04-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7145	19832	32801	2.73	1.6E+00	BE697267.1	EST_HUMAN	RCO-CT0415-200700-032-ct0 CT0415 Homo sapiens cDNA
7929	20824		1.19	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8277	20971	34112	3.28	1.6E+00	AJ287131.1	NT	Mus musculus SIL, MAP_17, GYP_a, SCL & GYP_b genes
8798	21490	34636	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8798	21490	34637	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21650	34810	0.47	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608647 5'
9360	25121	33549	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9360	25121	33550	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9487	22140		0.68	1.6E+00	AF043468.1	NT	Thermococcus ethanolicus D-xylase-binding protein (xyf) gene, complete cds
9634	22266	35480	1.32	1.6E+00	T41280.1	EST_HUMAN	ph668_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph668_19/1TV
10047	22695	35911	0.5	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase (aL), and zinc finger protein (DNZ1) genes, complete cds
10085	22733	35947	1.15	1.6E+00	AW856844.1	EST_HUMAN	QV4L1T0016-090200-100-407 L1T0016 Homo sapiens cDNA
10085	22733	35948	1.15	1.6E+00	AW856844.1	EST_HUMAN	QV4L1T0016-090200-100-407 L1T0016 Homo sapiens cDNA
10242	22850	36102	0.47	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	36305	0.45	1.6E+00	AF162084.1	NT	Glugea plecoglossi beta-tubulin 2 (btub2) gene, partial cds

Table 4

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10870	23361	36602	1.85	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10728	23416	36657	1.27	1.6E+00	AA216387.1	EST_HUMAN	nc16002.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008287 similar to contains element MER4 repetitive element;
10747	18612	31543	5.27	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
11705	24300	37628	3.48	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12889	25476	5.31	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25674	2.2	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 84 of the complete genome
606	13384		2.03	1.5E+00	6782861	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2518	15235	27975	2	1.5E+00	6078350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3368	16127	28785	0.72	1.5E+00	AE001845.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5642	18437	31350	0.83	1.5E+00	AB55301.1	EST_HUMAN	tt1210.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1;
5642	18437	31351	0.83	1.5E+00	AB55301.1	EST_HUMAN	tt1210.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1;
6312	19083	32068	3.02	1.5E+00	R17878.1	EST_HUMAN	XQ10602.1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:31693 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887555 5'
7060	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7060	19751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7245	19930	33006	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak28f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7493	20165	33257	0.76	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684693 3' similar to gb:395936 SEROTRANSFERRIN PRECURSOR (HUMAN);
7727	20380		0.64	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8021	20716	33848	0.89	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02138.1	NT	Mouse geminine IgM chain gene, mu-delta region
8914	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34876	0.46	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085135 5'
9383	22045	35217	0.84	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147697 5'
9635	22188	35374	1.39	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261059-008-d09 CT0192 Homo sapiens cDNA
9760	22411	35618	6.39	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150800-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF37944.1	EST_HUMAN	602035771F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4183865 5'
10098	22744	35958	1.66	1.5E+00	AA017688.1	EST_HUMAN	ze389g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'

Page 19 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10088	22744	35959	1.66	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:361306 5'
11375	23982	37282	4.46	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P243 3'
11630	24130		6.55	1.5E+00	X07380.1	NT	Malze mitochondrial RNA-Ser gene and tRNA-Phe pseudogene
11628	24226	37549	2.1	1.5E+00	A400798.1	EST_HUMAN	tg94d09.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11628	24226	37550	2.1	1.5E+00	A400798.1	EST_HUMAN	tg94d09.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12445	24815		3.38	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
28	12856	25472	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	12856	25473	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2333	15057		6.92	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2875	15384	28126	2.21	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2776	15481	28221	2.61	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2776	15481	28222	2.61	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4545	17280		1.81	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4297556 5'
5288	18053	30754	1.61	1.4E+00	AW054976.1	EST_HUMAN	wt45g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5441	18240		6.67	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6186	18953	31936	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6318	19089	32074	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	19089	32075	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
7186	19872	32946	2.07	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7201	19887	32952	1.17	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7258	18942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7268	18942	33019	0.76	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8233	20927		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8991	21681	34829	1.73	1.4E+00	R20459.1	EST_HUMAN	yg33f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9097	21785	34951	4.65	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9131	21819	34956	0.51	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds

Page 20 of 536  
Table 4  
Single Exon Probes Expressed In Brain

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10108	22756	35988	0.79	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	22769	36015	0.61	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10151	22769	36016	0.61	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10424	23070	36291	1.06	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	36292	1.06	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23675	36931	1.34	1.4E+00	AA195528.1	EST_HUMAN	z36609.1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:565612 5' similar to contains element MER22 repetitive element
11188	23853	37139	6.16	1.4E+00	AB006682.1	NT	Homo sapiens AP5CED mRNA for AIRE-1, complete cds
11381	23988	37288	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11391	23988	37289	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11404	24053	37358	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12078	26256		1.48	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
557	13339	26320	1.81	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
892	13651		3.42	1.3E+00	AJ271192.1	NT	Centhairellus sp. partial 28S rRNA gene, isolate Tibet
1107	13864		20.26	1.3E+00	Y19213.1	NT	Homo sapiens putative psihbA pseudogene for hair keratin, exons 2 to 7
1274	14024	26692	13.71	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1274	14024	26693	13.71	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Colx lacryme-jabi dihydrodipicolinate synthase (dapA) gene, complete cds
1605	14351		2.27	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2239	14967		1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2405	15126	27862	1.27	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2553	15288		1.75	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915946 3'
2940	15705	28334	0.73	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spnat1), mRNA
3584	16339	28984	0.89	1.3E+00	AF010494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5427	18226	30938	1.09	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5622	18418	31330	0.6	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
5893	18650	31590	0.81	1.3E+00	BF683825.1	EST_HUMAN	602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5'
5928	18712	31697	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-281199-004-f08 CT0289 Homo sapiens cDNA

Page 21 of 536  
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Single Exon Probes Expressed in Brain

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5928	18712	31688	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-008 CT0289 Homo sapiens cDNA
6323	18093	32081	1.34	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6652	19414	340166	0.76	1.3E+00	Q00186	SWISSPROT	HYPOTHETICAL GENE 84 PROTEIN
6739	19573	32606	0.62	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
6894	18954	32584	1.17	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7000	19692	32743	0.81	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7358	20039	33117	1.01	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8197	20891	34029	1.28	1.3E+00	AJ009912.1	NT	Sue scrofa pip gene
8346	21039	34178	2.78	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8459	21161	34294	0.86	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303	34525	1.78	1.3E+00	9910247	NT	Homo sapiens GLD04 protein (GLD04), mRNA
8689	21381	34525	0.79	1.3E+00	A927628.1	EST_HUMAN	w685a07 x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9415	22093	35273	6.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.56	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9424	22102	35274	2.66	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9524	22177	35361	0.96	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9569	22222	35407	1.58	1.3E+00	Q00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9651	22303	35498	1.14	1.3E+00	A927628.1	EST_HUMAN	w685a07 x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9726	22377	35578	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
9728	22377	35579	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
9766	22417	35624	4.63	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
9826	22477		0.48	1.3E+00	A1559944.1	EST_HUMAN	1q77a12.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb.X14723
10050	22698	35913	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10050	22698	35914	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	36974	1.62	1.3E+00	A5004392.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10130	22778	35991	1.35	1.3E+00	M29953.1	NT	Campylobacter jejuni kenamycin phosphotransferase (ephA-7) gene, complete cds
10483	23129		0.82	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
10511	23157	36383	0.45	1.3E+00	A1690848.1	EST_HUMAN	w632e10 x1 NCL_CGAP_GCB Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
10592	23286		4.6	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

Page 22 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	38744	1.93	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10846	23528	38772	2.01	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11307	23966		1.8	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCL CGAP_HNB Homo sapiens cDNA clone IMAGE:27398868 3'
11527	24127	37433	3.21	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.8kb fragment
12210	24875		2.64	1.3E+00	AF187873.1	NT	Caixa porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12388	24780	31035	6.3	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158462 5'
12397	25153		2.73	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	24848		2.15	1.3E+00	AF187035.1	NT	Stunira liliun cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
835	13414	26050	11.05	1.2E+00	AA876246.1	EST_HUMAN	z122408.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:431636 3'
804	13576	26239	0.87	1.2E+00	P08228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26240	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26241	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13627		1.35	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1138	13893	26554	6.64	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1183	13935	26600	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26601	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15873	28512	1.24	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15926	28573	5.88	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15926	28574	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3280	16041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3699	16452	29091	6.69	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3967	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MRQ-FT0176-050800-203-g06_1 F10175 Homo sapiens cDNA
4266	16110	28768	1.11	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4438	17174		1.67	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4487	17222	28850	0.98	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17259	29892	1.89	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4548	17283		6.43	1.2E+00	Y09200.1	NT	T. pinnae chloroplast rbcL gene, partial
5351	18134	30838	1.1	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5467	18268	31158	1.91	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6060	18840	31801	2.51	1.2E+00	X74885.1	NT	D. hydei ay1 repeat cluster DNA, fragment D
6119	18897	31865	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-190-a03 BN0090 Homo sapiens cDNA

Page 23 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6198	18974	31951	1.54	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6198	18974	31952	1.54	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6241	19015	31989	39.54	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Scores_teste_NHT Homo sapiens cDNA clone 1322374 3'
6342	19112	32101	0.55	1.2E+00	N33295.1	EST_HUMAN	y38b12.s1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273589 3' similar to gbIM878351HUMAALU472 Human carcinoma cell-derived Alu RNA transcript, (RNA), gb.J04970
6408	19177	32175	0.68	1.2E+00	P17671	SWISSPROT	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6412	19180	32176	2.06	1.2E+00	AW813276.1	EST_HUMAN	ECDYSONE-INDUCIBLE PROTEIN E75-A
6815	19478	32498	1.17	1.2E+00	AB028010.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6829	19490	32612	3.11	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7153	19840		0.94	1.2E+00	AJ271735.1	NT	Mus musculus DSPP gene
7282	25109	33044	4.86	1.2E+00	AV734585.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
7650	20220	33323	2.49	1.2E+00	XT4207.1	NT	AV734585 cda Homo sapiens cDNA clone cDAAFH03 5'
7603	20269	33378	0.56	1.2E+00	J05218.1	NT	L.lactis pyrD and pyrF genes
7715	20379	33492	0.56	1.2E+00	BE787646.1	EST_HUMAN	Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
8467	21159	34302	3.32	1.2E+00	AB033030.1	NT	601481781F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8501	21253	34391	0.68	1.2E+00	P38427	SWISSPROT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8775	21467		0.51	1.2E+00	7706271	NT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-GLUCOSEPHOSPHATE (TREHALOSE-6-PHOSPHATE SYNTHASE)
8923	21614	34758	1.87	1.2E+00	AW377210.1	EST_HUMAN	GLUCOSYLTRANSFERASE
9138	21826	34991	0.5	1.2E+00	H48599.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9298	21965	35138	3.76	1.2E+00	Z32850.1	NT	MR2-C10222-201099-001-e07 C10222 Homo sapiens cDNA
9505	22168	35339	1.81	1.2E+00	D11745.1	EST_HUMAN	yq80a06.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202068 6'
9831	22482	35684	2.86	1.2E+00	X59832.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
10224	22872		0.73	1.2E+00	AB009666.1	NT	HUMH01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo01a01
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	H.sapiens ENO3 gene for muscle specific enolase
11435	24045		10.62	1.2E+00	BE160761.1	EST_HUMAN	Homo sapiens kldho gene, exon 1
11435	23202	36434	4.36	1.2E+00	U50147.1	NT	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
12179	25227	30817	17.08	1.2E+00	AL163203.2	NT	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
12199	24667		2.8	1.2E+00	AP001515.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
451	13237	25876	1.53	1.1E+00	D85980.1	NT	Homo sapiens chromosome 21 segment HS21C003
1757	14499	27200	1.33	1.1E+00	AW995393.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 9/14
1892	14629	27339	0.98	1.1E+00	AW575889.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
							QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
							UI-HF-BR0p-ajk-f-02-0-J1.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

Page 24 of 538  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3480	16236	28892	1.11	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	16322	28970	1.01	1.1E+00	AI806360.1	EST_HUMAN	wf54h11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3707	16460	29086	1.05	1.1E+00	AE003886.1	NT	SW:P531_HUMAN Q12868 P53-BINDING PROTEIN 53BP1 ;
3707	16460	29089	1.05	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3798	16550		1.02	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4190	16931		5.69	1.1E+00	5835331	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4634	17389		0.81	1.1E+00	U34992.1	NT	R. unicornis complete mitochondrial genome
4934	17682	30272	3.45	1.1E+00	U18466.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
4935	17683	30273	1.05	1.1E+00	AJ271740.1	NT	African swine fever virus, complete genome
5129	17847	30484	1.07	1.1E+00	6880080	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5224	18031	30657	1.39	1.1E+00	6978530	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5526	18324	31226	16.75	1.1E+00	BE860184.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5545	18342	31260	1.2	1.1E+00	AI138582.1	EST_HUMAN	60165276R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825533 3'
6001	18782	31743	1.1	1.1E+00	11419739	NT	qd85c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6181	18998	31832	0.62	1.1E+00	AF187861.1	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6313	19084	32069	0.82	1.1E+00	R06037.1	EST_HUMAN	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6816	19379	32394	0.72	1.1E+00	AJ404004.1	NT	ye88e03.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
7155	19842	32956	0.58	1.1E+00	AF101091.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7196	19882	32956	0.72	1.1E+00	X55981.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7389	20068	33146	2.18	1.1E+00	Z72338.1	NT	Maize mRNA for enolase (2-phospho-D-glycerate hydratase)
7389	20068	33147	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7411	20088	33172	8.84	1.1E+00	AL161586.2	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7480	25115	33247	0.8	1.1E+00	11967960	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8032	20727	33860	3.01	1.1E+00	BF693986.1	EST_HUMAN	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8120	20814	33950	0.64	1.1E+00	AI476339.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8636	21328	34471	0.71	1.1E+00	AB003088.1	NT	tm39h11.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8714	21406	34549	0.75	1.1E+00	S80750.1	NT	Acetabularia calliculus mitochondrial COX-like gene
							VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]

Page 25 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	21516	34661	0.45	1.1E+00	A1079946.1	EST_HUMAN	cc24105.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		0.69	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35366	0.63	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9660	22233		1.2	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9672	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22383	35585	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
9837	22488	36690	4.59	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36260	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23160	36375	0.73	1.1E+00	A1878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618292 5' similar to gb:D10522
10547	23243	36478	2.25	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN):
10606	23300		3.1	1.1E+00	AF068942.1	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
11023	23695	36958	1.28	1.1E+00	11439558	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11026	23698	36961	1.58	1.1E+00	L16877.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11042	17901		6.23	1.1E+00	8922873	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11048	23718	36988	3.68	1.1E+00	AF012862.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36988	3.68	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11328	24016	37323	4.58	1.1E+00	A1809699.1	EST_HUMAN	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11561	24160	37470	1.63	1.1E+00	D89501.1	NT	wf76a11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11561	24160	37471	1.63	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12163	24639		3.66	1.1E+00	P07868	SWISSPROT	Human PBI gene, complete cds
12250	24697	31078	1.93	1.1E+00	AF216698.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12378	26225		2.09	1.1E+00	AF234169.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12388	25200		1.44	1.1E+00	8393196	NT	Dicotyledonous discoidium isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
97	12923		2.46	1.0E+00	U23808.1	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Crp), mRNA
111	12932	25569	0.73	1.0E+00	D88425.1	NT	Xenopus laevis rhodopsin gene, complete cds
409	13194		2.25	1.0E+00	AB021684.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
562	13344	25971	1.2	1.0E+00	AJ251660.1	NT	Marchantia polymorpha genes for 28S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
662	13438	26079	4.38	1.0E+00	AL163218.2	NT	Gliardia ligaria mRNA for homeodomain transcription factor (so gene)
							Homo sapiens chromosome 21 segment HS21C018

Page 26 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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663	13439		0.95	1.0E+00	AF126984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1366	15567		3.03	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1751	14493	27193	0.93	1.0E+00	AB008531.1	NT	Plautia stali Intestine virus RNA for nonstructural
2489	15206	27947	1.18	1.0E+00	P48355	SWISSPROT	polyprotein, capsid protein precursor, complete cds
2489	15206	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
							DNA GYRASE SUBUNIT B
2878	15845	28287	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15845	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2897	15733		1.17	1.0E+00	O14226	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3194	15957	28609	1.24	1.0E+00	AA628453.1	EST_HUMAN	ar26g08.s1 Sceres_tale Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3585	12923		1.24	1.0E+00	U23808.1	NT	WP:CA2D8.3 CE04204 ; contains element MER22 MER22 repetitive element ;
3689	16422	28063	1.04	1.0E+00	AJ23816.1	NT	Xenopus laevis rhodopsin gene, complete cds
							Agaricus bisporus mRNA for tyrosinase
4050	16795	29424	0.76	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4242	16983		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4954	17680		0.93	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
4975	17698	30306	0.74	1.0E+00	AF092505.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds, and proximal Rump white inversion breakpoint
5200	18008	30629	3.53	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551	31472	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5759	18551	31473	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5987	18654	31595	1.53	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6024	18804	31765	4.7	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	UI-H-B13-ak-d-09-0-UI.s1 NC1 CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6397	19169	32168	1.95	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6447	19215	32213	0.91	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6534	19300		1.08	1.0E+00	P48506	SWISSPROT	SRB-11 PROTEIN
6879	19596	32634	1.33	1.0E+00	Y11204.1	NT	V. carteri gene encoding veloxapsin

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7038	19730	32788	1.09	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058		9.29	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7611	20277	33385	1.56	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7628	20292	33401	5.26	1.0E+00	AA775191.1	EST_HUMAN	ac79808.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:888781 3'
7661	20558	33681	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7661	20558	33682	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8041	17680		1.19	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8248	20942	34079	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34080	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8378	21069		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8408	21101	34237	0.5	1.0E+00	Q9Y575	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8408	21101	34238	0.5	1.0E+00	Q9Y575	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8438	28122		2.34	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181089-011-e08 HT0229 Homo sapiens cDNA
8478	21168	34312	0.88	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8625	21317	34459	1.27	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9171	21841	35008	2.43	1.0E+00	BE507592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clcat1), mRNA
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clcat1), mRNA
9510	22163	35345	1.83	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK C Homo sapiens cDNA clone GKCCYA11 5'
9516	22169	35351	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9516	22169	35352	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds

Page 28 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9753	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9753	22404	35610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35876	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10012	22660	35876	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10104	22752	35968	0.81	1.0E+00	A1077920.1	EST_HUMAN	oy1607.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10225	22873	36085	4.36	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10375	23021	36237	16.18	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10375	23021	36238	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10407	23053	36270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10893	23573	36823	4.57	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 888 nt]
11025	23697	36960	1.49	1.0E+00	AA701494.1	EST_HUMAN	z63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element ;
11522	24122		1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18008	30629	1.55	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11838	24422	37793	12.29	1.0E+00	Q60019	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11868	24452	37794	1.38	1.0E+00	9826187	NT	Human adenovirus type 5, complete genome
12049	24568		3.01	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772		2.32	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGI resequences, MAGN Homo sapiens cDNA
2843	15353	28097	1.19	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3591	16345		0.97	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5547	18344	31253	10.09	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
5779	18570	31498	0.93	9.9E-01	Q09832	SWISSPROT	PROBABLY OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9160	21830		1.37	9.9E-01	U65667.1	NT	Lycopodium esculentum putative M11 copy 1 nematode-resistance gene
9455	22005		2.18	9.9E-01	Q26642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10814	23308	36547	2.37	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Epi-like receptor tyrosine kinase rtk8
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B.aphidicola 16S rDNA (host T. suber)
11592	24191	37509	2.3	9.9E-01	Y11972.1	NT	B.aphidicola 16S rDNA (host T. suber)
510	13294	25928	1.14	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	16020		1.21	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	16509		1.01	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3781	16533	29171	0.82	9.8E-01	O87551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV)
7089	19788	32852	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

Page 29 of 536  
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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7099	19788	32853	4.87	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33316	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7646	20216	33317	1.16	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8819	21311	34453	0.91	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10336	22983		1.13	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23596	36842	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
10918	23598	36843	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
11764	24355	37688	1.57	9.8E-01	A680876.1	EST_HUMAN	bx42c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12256	24702		1.56	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7058	18749	32812	2.28	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, o, d and e, partial cds
8401	21084	34230	1.68	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8407	21100	34236	1.3	9.7E-01	M80544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11123	23792		3.64	9.7E-01	BF511209.1	EST_HUMAN	UI-H-B14-sol-e-07-o-UI.s1 NCI_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3085140 3'
4425	17161	29791	1.5	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5687	18462	31376	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5687	18462	31377	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6848	18410	32424	0.61	9.6E-01	Z97341.2	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
8291	20985		2.33	9.6E-01	X96275.1	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8760	21442	34589	0.59	9.6E-01	L81138.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
11503	24104	37416	3.47	9.6E-01	AV752605.1	EST_HUMAN	Rattus norvegicus (strain R21) Rps21 gene, complete cds
11503	24104	37417	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11952	24505		1.92	9.6E-01	11421722	NT	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
2480	16198	27698	1.05	9.6E-01	7705591	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2673	15382	28122	0.87	9.5E-01	Q02894	SWISSPROT	Homo sapiens CGI-125 protein (LOC31003), mRNA
3762	16514	28150	2.04	9.5E-01	BE802340.1	EST_HUMAN	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I)
3762	16514	28151	2.04	9.5E-01	BE802340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8899	21950	34730	0.89	9.5E-01	A180162.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9003	21893	34843	1.05	9.5E-01	AW861102.1	EST_HUMAN	qd57407.x1 Soares_bas1s_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
							RC1-CT0295-241198-011-502 CT0295 Homo sapiens cDNA

Page 30 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11209	23872	37189	1.68	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4103630 5'
11428	23196	36427	2.42	9.5E-01	AW283789.1	EST_HUMAN	UI-H-B12-ahp-f-03-q-UJ.st NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11795	24385	37718	1.55	9.5E-01	T67204.1	EST_HUMAN	ys53d04.st Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:66631 3'
3186	15959		3.33	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (pcB) gene, partial cds
3212	15975		2.08	9.4E-01	AF080595.1	NT	Plimphella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34606	0.87	9.4E-01	M80724.1	NT	Human Fe-gamma-receptor1A (FCGR2A) gene, exon 4
12202	24670		1.92	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
12557	25219		1.79	9.4E-01	11418857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1726	14468		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytoeyl-CoA hydroxylase (PHYH) gene, exon 5
2640	15351	28095	1.36	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4015	16761	28388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	28389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5505	18303	31204	1.56	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18388	31298	3.89	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7966	20661	33785	1.65	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.st NCL CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8835	21827	34673	0.95	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24970		3.12	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl.34 mRNA, complete cds
12802	25049		1.48	9.3E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticlin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
3233	15995	28648	2.83	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184.3'
4922	17553		0.97	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5931	18428		1.15	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6898	18983	31631	7.36	9.2E-01	BF037686.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864681 5'
6537	19302	32308	0.81	9.2E-01	M84703.1	NT	N.crassa valyl-tRNA synthetase (cyc-20/un-3) gene
9560	22213	35399	0.92	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9548	22300	35496	1.07	9.2E-01	6671677	NT	Arabidopsis thaliana DNA chromosome 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430983	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22962	36178	1.9	9.2E-01	BF593251.1	EST_HUMAN	7c58a06.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10543	23239	36473	1.63	9.2E-01	BE5563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;

Page 31 of 536  
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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24316	37639	1.79	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1621	14368	27087	1.88	9.1E-01	T98876.1	EST_HUMAN	y55201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
2120	14851		2.76	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15063	28814	1.15	9.1E-01	T26418.1	EST_HUMAN	AB20036R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3200	15963	28815	1.15	9.1E-01	T26418.1	EST_HUMAN	AB20036R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6075	18954	31821	1.28	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6413	19181	32180	3.53	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7475	20148	33241	17.62	9.1E-01	AA806623.1	EST_HUMAN	cb71908.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7637	20302	33410	2.34	9.1E-01	U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10076	22723	35940	0.45	9.1E-01	P38432	SWISSPROT	P80-COILIN
12291	25294		27.98	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4346	17085	29714	2.08	9.0E-01	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
7291	19974	33052	0.72	9.0E-01	L42847.1	NT	Danio rerio LIM class homeodomain protein (lim6) mRNA, complete cds
7321	20004		1.18	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds
9249	21928	35100	0.49	9.0E-01	AF088761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
5610	18406	31318	2.68	8.9E-01	AF026108.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6154	18931		1.38	8.9E-01	X60086.1	NT	Rabbit MHC fragment RLA-DF DNA
8325	21018	34154	0.71	8.8E-01	AF259667.1	NT	Oithona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
11787	24377	37707	2.51	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12138	24827		2.86	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
12762	25343		2.51	8.9E-01	AI150836.1	EST_HUMAN	qb64408.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1704879 3'
4505	17240	28873	3.82	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
6289	18094	30755	0.67	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22778	35992	0.83	8.8E-01	7656878	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23690	36953	4.96	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11968	26382		1.8	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1718643
432	13238	25877	1.54	8.7E-01	AF100853.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	16644	28286	5.05	8.7E-01	AA595863.1	EST_HUMAN	nm05f11.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
4946	17673						Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5102	17820		3.17	8.7E-01	AF121970.1	NT	Homo sapiens partial LGALS9 gene for galactin-9, exon 3
7939	20634		0.97	8.7E-01	AJ288085.1	NT	RC4-NN0057-120500-073-c07 NN0057 Homo sapiens cDNA
8828	21520	33761	0.92	8.7E-01	AW897335.1	EST_HUMAN	q136e06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1848786 3'
8828	21520	34665	0.69	8.7E-01	AJ239456.1	EST_HUMAN	q136e06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1848786 3'
8828	21520	34668	0.69	8.7E-01	AJ239456.1	EST_HUMAN	q136e06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1848786 3'
9638	22290	35483	1.57	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10202	22850	36065	0.61	8.7E-01	BF570169.1	EST_HUMAN	802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'
10202	22850	36066	0.61	8.7E-01	BF570169.1	EST_HUMAN	802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'
10735	23422	36665	5.25	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	5.47	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
462	13247		1.76	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
838	13608	26279	3.45	8.6E-01	W69089.1	EST_HUMAN	zf44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2268	14994	27733	0.96	8.6E-01	4603210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3608	16361	29003	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3782	16534	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5808	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5808	18597	31525	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6809	19372	32385	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6809	19372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104	32388	2.06	8.6E-01	AF143732.1	NT	Helicobacter pylori 26895 section 69 of 134 of the complete genome
7427	20104	32388	2.06	8.6E-01	AF143732.1	NT	Helicobacter pylori 26895 section 69 of 134 of the complete genome
7828	20523		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7941	20938	33763	0.55	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9585	22238		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12518	25144		0.78	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6628	19388	32401	1.35	8.6E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7426	21012	33189	2.51	8.5E-01	BE542612.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8317	21010	34147	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8317	21010	34148	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Page 33 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22898	36105	1.17	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10248	22898	36108	1.17	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12278	28298		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
4702	17438	30087	0.73	8.4E-01	AF083976.2	NT	Fowl adenovirus 8, complete genome
5406	25068	30910	2.28	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25088	30911	2.28	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF061142.1	NT	Manestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
9858	22508		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
724	13498	26161	2.8	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	16866	28497	2.99	8.3E-01	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3780	16542	28177	0.78	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3893	16741	28376	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17995	30511	2.41	8.3E-01	AL161640.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9568	22221		4.51	8.3E-01	A791852.1	EST_HUMAN	nm011212, x5 NCI CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element;
10010	22658	35872	1.27	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10118	22766	35978	3.48	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10572	23267	36505	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283408 (section 109 of 148) of the complete genome
10590	23284		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	23835	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145689.1	NT	Mus musculus trophalin (Tnn) gene, complete cds
2686	16395		1.08	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
6876	19593	32631	0.75	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
6797	19541	32569	3.49	8.2E-01	AW376993.1	EST_HUMAN	CM4-HT0243-081189-037-e01 HT0243 Homo sapiens cDNA
7189	25108	32926	4.74	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8343	21038	34173	0.59	8.2E-01	BE263145.1	EST_HUMAN	60114488F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9924	22572	35770	0.65	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9959	22607	35812	1.37	8.2E-01	AF052859.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10123	22771	35885	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35986	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1

Page 34 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10283	22931	36146	3.85	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22931	36146	3.85	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11641	24238	37562	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328	37562	6.38	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	6.02	8.2E-01	H87398.1	EST_HUMAN	hw1402.1 Soares_placentia_8609weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:262195 5'
12288	24723	31054	2.37	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2762	15467		1.08	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3451	16207	28857	3.08	8.1E-01	AF055086.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207	28858	3.08	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
4663	17592		0.74	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
6223	18997	31973	0.84	8.1E-01	U16790.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6226	19292	32295	2.66	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6526	19292	32296	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7229	19914	32987	0.78	8.1E-01	AB007877.1	NT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7412	20089	33173	0.65	8.1E-01	Q47477	SWISSPROT	Homo sapiens KIAA0417 mRNA, complete cds
							CYTCHROME B
7811	20506	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
7811	20506	33629	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8507	21189	34344	0.93	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21189	34345	0.93	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							xr01h03.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW:LYAR_MOUSE
8668	21360	34507	1.08	8.1E-01	AW242647.1	EST_HUMAN	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, ;contains MER22 b1 P TR5, repetitive element;
10026	22673	35888	0.7	8.1E-01	P08425	SWISSPROT	PROBABLE E4 PROTEIN
10311	22958	36174	0.5	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
11464	24067	37374	2.63	8.1E-01	BE938558.1	EST_HUMAN	EST(CLONE C-0PE11)
11464	24067	37375	2.63	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12022	24550	31110	1.57	8.1E-01	AE001711.1	NT	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
172	12985		3.49	8.0E-01	AJ271510.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
							Staphylococcus aureus partial pla gene for phosphatase allele 15

Page 35 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psmr1), mRNA
2029	14764		1.91	8.0E-01	BF530862.1	EST_HUMAN	602072473F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3076	15841	28484	1.2	8.0E-01	AF127897.1	NT	Salmid boliviensis olfactory receptor (SBO27) gene, partial cds
3307	16067	28716	1.39	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3690	16443		1.52	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 777
4498	17232	29862	6.05	8.0E-01	X83739.2	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7889	20584		2.25	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8423	21116	34254	0.98	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10878	23558	36803	2.78	8.0E-01	Q92783	SWISSPROT	CREB-BINDING PROTEIN
441	13227	25870	1.16	7.9E-01	D11478.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	13473		1.14	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1600	14346		22.69	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
1652	14398		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2269	14988	27726	5.66	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2260	14987	27727	2.4	7.9E-01	AF130459.1	NT	Danio rerio Tnp4-associated protein Tap1A (tap1A) mRNA, complete cds
3506	16262	28916	3.01	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4288	17008		0.85	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4572	17307	29835	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4672	17307	29836	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
6252	19026	32000	0.67	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33831	2.79	7.9E-01	X90986.1	NT	P. sativum GR gene
9447	22124	35304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9949	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9991	22639	35849	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GK Homo sapiens cDNA clone GKCDRE12 3'
10408	23054	36271	1.94	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10516	23162	36389	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10929	23609		2.74	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	37123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
858	13826		2.24	7.9E-01	Z43765.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2273	14999	27737	7.47	7.9E-01	AW950567.1	EST_HUMAN	EST T371637 MAGF resequences, MAGF Homo sapiens cDNA
4653	17387	30020	0.73	7.9E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5978	18760	31724	2.28	7.9E-01	AF115858.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31871	0.88	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON
6371	19140	32136	0.63	7.8E-01	AL445066.1	NT	BETA-2) (HYBRIDOMA GROWTH FACTOR)
8389	21082	34216	1.02	7.8E-01	BF108927.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5
9133	21821	34987	1.3	7.8E-01	Y10159.1	NT	7154405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9231	21810	35083	0.51	7.8E-01	4828873	NT	D.discoideum recGAP gene
10024	22872		0.87	7.8E-01	Q25462	SWISSPROT	Homo sapiens nucleoprotein 214kD (CAIN) (NUP214), mRNA
12271	25273		2.5	7.8E-01	L29260.1	NT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
139	12854	25596	7.61	7.7E-01	AF184346.1	NT	Arabidopsis thaliana 1-aminocyclopropanecarboxylate synthase (ACS5) gene, complete cds
709	13483		2.28	7.7E-01	AF050157.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
2717	15424	28163	2.21	7.7E-01	Q33915	SWISSPROT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aelpha) and major histocompatibility protein class II beta chain (Ilebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-IP
3351	16111		0.84	7.7E-01	8393408	NT	CITRATE SYNTHASE
3686	16340	28985	3.98	7.7E-01	AF118085.1	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
4365	17103	29738	3.38	7.7E-01	AF199488.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4365	17103	29739	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31165	1.45	7.7E-01	P16553	SWISSPROT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31168	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5868	18553	31594	0.85	7.7E-01	R08600.1	EST_HUMAN	RAFFINOSE INVERTASE (INVERTASE)
8744	22395	35800	0.51	7.7E-01	AB021134.1	NT	y24b02.s1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:127765 3'
12161	24844		4.55	7.7E-01	11497621	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
6008	18789	31751	4.88	7.6E-01	AF059510.1	NT	Archaeoglobus fulgidus, complete genome
6008	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6426	18193	32189	0.81	7.6E-01	P37938	SWISSPROT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6751	17920	30555	0.94	7.6E-01	A1253399.1	EST_HUMAN	MATING-TYPE PROTEIN A-ALPHA Z4
6751	17920	30585	0.94	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6951	19433	32449	0.88	7.6E-01	U72487.1	NT	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
							Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7984	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HBAR (Hbar) gene, complete cds
8026	20721	33852	1.88	7.6E-01	6857752	NT	Mus musculus edvillin (Advil-pending), mRNA
8026	20721	33853	1.88	7.6E-01	6857752	NT	Mus musculus edvillin (Advil-pending), mRNA
8866	21557	34703	0.74	7.6E-01	6753577	NT	Mus musculus aduillin (Advil-pending), mRNA
9179	21849	35015	5.03	7.6E-01	P30372	SWISSPROT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.68	7.6E-01	X86347.1	NT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37326	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11711	24306		3.64	7.6E-01	AL161592.2	NT	H. aspersa mRNA for neurofilament NF70
11831	24489		3.73	7.6E-01	AB020702.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
500	13284		1.44	7.6E-01	AL163301.2	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
570	13351	25979	1.23	7.6E-01	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C101
3354	16114	28769	0.95	7.6E-01	C14203.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7421	20098	33186	1.01	7.6E-01	AF052730.1	NT	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
11177	23844	37130	1.5	7.6E-01	AB047819.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12228	24682		4.8	7.6E-01	AF163161.2	NT	Homo sapiens GCMa/GCM1 gene for chorion-specific transcription factor GCMa, complete cds
12742	25008	30975	1.46	7.6E-01	AE000823.1	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
1108	13865	26522	1.78	7.4E-01	AI598146.1	EST_HUMAN	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
2342	15065	27802	0.86	7.4E-01	AB011106.1	NT	tnt4b09.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element
4276	17015	28642	4.73	7.4E-01	AL163246.2	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
7743	20439	33562	1.23	7.4E-01	AL161551.2	NT	Homo sapiens chromosome 21 segment HS21C046
7743	20439	33563	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
8531	21223	34365	0.83	7.4E-01	BF346268.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8613	21305		0.76	7.4E-01	U87960.1	NT	602018456F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4164340 5'
8994	21694	34834	6.95	7.4E-01	BE747503.1	EST_HUMAN	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9054	21743	34901	1.14	7.4E-01	AA187988.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
10302	22849	36164	0.76	7.4E-01	11424933	NT	zp87h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:825297 3' similar to SW:TCQP_MOUSE P42982 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
							Homo sapiens NY-REN-45 antigen (LOC51133), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11665	24260	37582	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11669	24260	37583	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11900	24467		3.62	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1ih), mRNA
12008	24542		1.78	7.4E-01	AK472641.1	EST_HUMAN	lat3h01.x1 NCL CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
2999	16765	28413	0.8	7.3E-01	P09710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (IRL1) (TRL1)
4575	17310	29938	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4652	17386	30019	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5040	17759	30373	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6511	19276	32278	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6511	19276	32277	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6894	25103	32735	0.67	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7369	20040	33118	0.66	7.3E-01	Z14133.1	NT	D.melanogaster Cdc mRNA for clathrin heavy chain
7445	20121	33210	0.84	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7445	20121	33211	0.84	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11407	24066	37361	3.83	7.3E-01	AA678019.1	EST_HUMAN	225608.s1 Soares_fetal_liver_spleen_INFIL5_S1 Homo sapiens cDNA clone IMAGE:431795 3'
11407	24066	37362	3.83	7.3E-01	AA678019.1	EST_HUMAN	225608.s1 Soares_fetal_liver_spleen_INFIL5_S1 Homo sapiens cDNA clone IMAGE:431795 3'
812	13583		3.89	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1950	14685	27398	2.32	7.2E-01	X79140.1	NT	N.laticum Nelf-4A13 mRNA
2463	15181	27920	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3063	15829	28473	1.38	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3445	16201	28851	2.56	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3601	16364	28994	1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4040	16785		0.7	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4718	17450	30083	2.65	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5075	17794	30410	0.74	7.2E-01	P33066	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
7112	19800	32864	0.88	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8353	21046	34183	1.11	7.2E-01	AF236061.1	NT	Oryzotegus cuniculus RING-finger binding protein mRNA, partial cds
8892	21553		0.46	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10239	22897	36100	2.33	7.2E-01	BF670081.1	EST_HUMAN	602116381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276381 6'
10639	23330	36568	4.02	7.2E-01	U92623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
11104	23774	37049	1.27	7.2E-01	S76838.1	NT	Dbs=Dbi guanine nucleotide exchange factor homolog [mouse, 32D murine hemopoietic cell line, mRNA, 3923 nt]

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12422	24788		2.8	7.2E-01	AP000053.1	NT	Aeropyrum pernix genomic DNA, section 6/7
676	13451	26094	12.73	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3059	16826	28470	11.76	7.1E-01	AJ270777.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 15-16
4184	16928	29555	3.18	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4184	16925	29556	3.18	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
5858	18645	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
5858	18645	31586	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
5850	19550	32580	7.68	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyl-tetrahydropterin synthase (pr) gene, complete cds
8091	20785	33916	0.56	7.1E-01	H54244.1	EST_HUMAN	y499d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202861 3'
8635	21327	34469	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
8635	21327	34470	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
9755	22406	35613	1.43	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898485 5'
10309	22959	36172	1.22	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-chain J2 gene
12211	25205		2.21	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1207	13958	26624	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1207	13959	26625	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
2450	15169	27907	1.13	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2450	15169	27908	1.13	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
4936	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5862	18649		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
6276	20870		11.76	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9216	21895	35064	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9216	21895	35065	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
10526	23172	36400	0.49	7.0E-01	U34662.1	NT	Danio rerio complement factor B mRNA, complete cds
11094	23734	37006	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11094	23734	37007	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
949	13715	26380	11.02	6.9E-01	U69874.1	NT	Candida albicans equalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

Page 40 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
949	13715	26381	11.02	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.9E-01	AA593330.1	EST_HUMAN	nm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213	15976	28927	1.97	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5694	18488	31409	0.91	6.9E-01	AB035562.1	NT	Branchiostoma belcheri BBN3 mRNA for notochord actin, complete cds
5900	18685	31633	0.82	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP50, partial
6277	19050	32027	1.36	6.9E-01	BE298188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7697	20360	33474	0.65	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
7878	20574	33701	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
9069	21758		0.79	6.9E-01	AF118048.1	NT	Entamoeba dispar: calion transporting ATPase (atpase) gene, partial cds
9594	22247	35431	0.59	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23886	37172	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11223	23886	37173	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11878	26197		3.01	6.9E-01	Q69958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
937	13704	26369	1.05	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2680	15389		0.99	6.8E-01	D90917.1	NT	Synochocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14356	27045	1.49	6.8E-01	AA854475.1	EST_HUMAN	aj76a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402266 3' similar to gb:X59411_ma1'ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4533	17268	29901	1.45	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
9538	22191	36376	1.45	6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23699	36962	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11027	23699	36963	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11058	23728	37001	2.4	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37527	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>

Page 41 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
281	13087	25739	44.11	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27806	1.73	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares, total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2163	15587	27628	2.51	6.7E-01	AF188073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2894	15760	28408	3.41	6.7E-01	6678560	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29786	0.79	6.7E-01	X74421.1	NT	Stibatorum mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30832	0.94	6.7E-01	JO4836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30833	0.94	6.7E-01	JO4836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	19005	31981	1.18	6.7E-01	8635035	NT	Galid herpesvirus 2, complete genome
6231	19005	31982	1.18	6.7E-01	8635035	NT	Galid herpesvirus 2, complete genome
7215	19900		4.34	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240	19925	33000	0.92	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.88	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23553	36800	2.07	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11436	23203	38435	3.59	6.7E-01	O14957	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11659	24255	37578	1.66	6.7E-01	AA342521.1	EST_HUMAN	EST 48065 Fetal spleen Homo sapiens cDNA 3' end
2505	15222	27964	1.29	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT1) mRNA, partial cds
2704	16411	28148	1.44	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	16403	29043	4.57	6.6E-01	Y07669.1	NT	C. albicans random DNA marker, 282bp
4089	19832		0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5125	17843	30461	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
6240	19014	31688	4.29	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7585	20263	33359	3.76	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8464	21156	34289	0.52	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9564	22217		2	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470	24836	31033	1.48	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
610	13388	26019	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

Page 42 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
610	13388	26020	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3428	16183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	16900	28615	4.23	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4277	17016	28643	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5003	17726	30329	2.6	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25087	30843	1.77	6.5E-01	P18480	SWISSPROT	(TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
5627	18424	31337	0.62	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6625	19387	32400	1.5	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7568	20236	33340	0.84	6.5E-01	A1798882.1	EST_HUMAN	wc48a02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321642 3'
9737	22388		0.8	6.5E-01	T78904.1	EST_HUMAN	yd21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10233	22881	36094	1.86	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10529	23226	36460	2.68	6.5E-01	H87583.1	EST_HUMAN	yw1706.r1 Soares_placenta_8to9weeks_2NbpHP808W Homo sapiens cDNA clone IMAGE:262516 5'
10585	23280	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	not15c07.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10690	23381		3.93	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11599	24198	37518	2.42	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12287	24710		2.07	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12504	25146		1.81	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
245	13054	25694	8.05	6.4E-01	U48848.1	NT	Orosophila melanogaster 8kd dynein light chain mRNA, complete cds
2593	15307	28043	1.16	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tryptophan halogenase (pmA) gene, complete cds
3449	10205	28855	2.16	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3842	16593	29230	1.08	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
8510	21202	34347	1.82	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
9899	22637	35848	8.6	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10004	22652	35884	1.22	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12382	24777		5.99	6.4E-01	AV769212.1	EST_HUMAN	AV769212 MDS Homo sapiens cDNA clone MDSGCG09 5'
425	13211	25858	4.58	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
522	13305	25938	2.25	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2159	14889	27623	2.02	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2583	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15297	28036	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds

Page 43 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5973	18765	31716	0.94	6.3E-01	BE033908.1	EST_HUMAN	PM0-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6504	19269	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8419	21112		3.44	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3969361 5'
8784	21478	34624	0.95	6.3E-01	S82927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9320	21987	35169	2.45	6.3E-01	9627621	NT	Varicella virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9838	22489		0.67	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10326	22873	36183	1.47	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36284	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	AW795395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
10993	23687	36924	2.21	6.3E-01	AA877715.1	EST_HUMAN	nm00008.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002918 002918 HLARK.
11308	23987	37288	9.25	6.3E-01	A1904160.1	EST_HUMAN	CM-BT043-080299-048 BT043 Homo sapiens cDNA
11402	24051	37355	1.66	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11581	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11888	25355	30607	4.37	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12078	24587		1.45	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12283	25272		2.93	6.3E-01	X8528.1	NT	C.limicola pecD gene
5780	19571	31489	2.31	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7394	20073		3.44	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (CaSR-rs4) mRNA, partial cds
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltracin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213542 3'
8765	21447	34595	0.52	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytochrome Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinolate dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9349	20420	33540	1.55	6.2E-01	BE562687.1	EST_HUMAN	601336148F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9410	22072		2.55	6.2E-01	M24461	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9878	22826	35834	6.2	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35982	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36308	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.38	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
6449	18248	31137	1.15	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6920	19556	32702	0.64	6.1E-01	AW105853.1	EST_HUMAN	xd50h03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7005	19897	32751	0.72	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8132	20826	33962	3.27	6.1E-01	AFD33353.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34528	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34529	1.09	6.1E-01	11431065	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21882	35153	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21882	35154	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22393	35597	0.93	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
9946	22594	35787	1.06	6.1E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11738	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30899	2.28	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
12694	24977		1.57	6.1E-01	X95287.1	NT	M. mazzel orfA, orfB, and orfC of archaeal ABC-transporter system
482	13287	25903	1.24	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
548	13331		3.09	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1341	14089	26765	1.91	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3785	16547	29180	0.92	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5189	18007	30628	2	6.0E-01	P20286	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18156	30839	2.86	6.0E-01	AW139713.1	EST_HUMAN	U1-HB11-eeb-a-10-O-UI.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6445	18213	32210	2.78	6.0E-01	U39813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

Page 45 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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6563	19328	32335	0.88	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW 136) (CD136 ANTIGEN)
7254	19338	33013	8.99	6.0E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8023	20718	33850	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8023	20718	33851	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22374	35574	1.61	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10173	22821		1.46	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10990	23684	36921	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10990	23684	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11540	24140	37449	3.77	6.0E-01	AK20623.1	EST_HUMAN	U0807.1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2095621 3'
12354	24758	31060	2.25	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12455	24824		2.6	6.0E-01	AA706087.1	EST_HUMAN	298905.s1 Soares fetal liver spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12639	25208	30815	3.04	6.0E-01	8055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12684	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	RC1-H10375-030500-015-c03 HT0376 Homo sapiens cDNA
980	13745	26407	1.36	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 18 of 163 of the complete genome
3264	16026	28675	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3264	16026	28676	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4196	16937		4.21	6.9E-01	AF162766.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
6373	19142	32139	1.55	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7166	19853	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7266	19979		0.61	5.9E-01	X68801.1	NT	G. gallus gene for skeletal alpha-actinin, exon EF2
7898	20593	33725	0.46	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
8536	21228	34370	0.48	5.9E-01	D12622.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9443	22120	35299	0.82	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUJW31/Cx major outer membrane protein (omp1) gene, complete cds
9813	22464		0.74	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10088	22736	35951	1.15	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHelial-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10569	23204	36502	2.5	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (TMP KINASE)
10576	23271	36507	1.72	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10881	23561	36808	2.91	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-003 DT0041 Homo sapiens cDNA
11149	23816	37099	1.95	5.9E-01	AF064626.1	NT	Mus spratus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11453	24082	37368	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11458	24062	37369	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
12021	24549	31109	2	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12252	24698		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12485	24832		5.72	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1902	14639	27348	1.36	5.8E-01	P40472	SWISSPROT	SM1 PROTEIN
2569	15283	28021	1.01	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	29838	4.37	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
5290	18095		0.82	5.8E-01	AE002162.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
6444	18243	31131	0.62	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18809	31835	1.09	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujliwara) Homo sapiens cDNA clone GEN-500E06 5'
6220	18994	31970	0.68	5.8E-01	D50601.1	NT	Shigella connei DNA for 28 ORFs, complete cds
6715	19630		2.48	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.61	5.8E-01	H41571.1	EST_HUMAN	Yn91003.s1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:176767 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
7885	20680	33806	0.64	5.8E-01	A1280051.1	EST_HUMAN	q185d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
7885	20680	33808	0.84	5.8E-01	A1280051.1	EST_HUMAN	q185d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8789	21481	34828	8.97	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8871	21582	34707	0.99	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
8872	21583	34708	0.51	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9486	22149		0.81	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
10911	23591	36837	7.56	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10962	23638		3.97	5.8E-01	BF700092.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11089	23759		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1480	14227	26912	1.12	6.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1480	14227	26913	1.12	6.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.69	5.7E-01	6755253	NT	Mus musculus plasminogen variant translocation 1 (Pvt1), mRNA
3217	15980	28631	1.62	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3495	16251		2.82	6.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6262	19036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	601454862F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3858580 5'
6811	19374	32388	0.81	5.7E-01	AA194201.1	EST_HUMAN	z38c08.11 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666874 5'
6763	17932	30568	1.33	6.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Page 47 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7664	20328	33438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
7670	20565		0.5	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tesc4 and Tesc6 genes, alternative transcripts
8279	20973		0.47	5.7E-01	AI065061.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
9689	22350	35544	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9699	22350	35545	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	36361	0.72	5.7E-01	BF540862.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068610 5'
11983	24524		1.52	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-e02 HT0736 Homo sapiens cDNA
12658	24958		3.01	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3367	16117	28772	1.3	6.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3367	16117	28773	1.3	6.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3863	16613	29252	0.97	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	16956	29578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21394	34541	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
8702	21394	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9275	22029	35189	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11884	24467		2.57	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11897	24535	37272	1.63	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12352	16613	29252	1.69	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12379	24776		2.7	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12773	25027		4.26	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	26606	0.85	5.6E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pcd), mRNA
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28150	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2919	15695	28330	1	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3082	15828		1.55	5.5E-01	H48219.1	EST_HUMAN	yol18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3228	15891	28644	4.22	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3678	16431	29073	1.7	5.5E-01	P48769	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.79	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
7187	16873		0.66	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	AI791766.1	EST_HUMAN	or62601.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9667	22319		0.7	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SFU 415/85 nucleoprotein gene, complete cds

Page 48 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	22624	36136	0.96	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stratagene (cat#38206) Homo sapiens cDNA clone HFBCQ35
11087	23757	37033	1.65	5.5E-01	BF128507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12955	25597	4.91	6.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
140	12955	25598	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
571	13352	25980	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
571	13352	25981	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1248	13997	26664	3.41	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-180-c04 NN0040 Homo sapiens cDNA
2099	14930		3.43	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2252	14980	27719	1.91	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-dlox gene)
5066	17785	30402	0.92	5.4E-01	M74439.1	NT	Rattus rattus UDP glucuronosyltransferase gene, complete cds
5571	18388	31278	0.74	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6098	18876	31845	0.83	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
6928	19684	32710	0.97	5.4E-01	BE966592.2	EST_HUMAN	601860276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906080 3'
7235	19920	32993	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7235	19920	32894	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7237	19922	32897	1.48	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE ]
9890	22540		2.09	5.4E-01	BF672536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11015	23687	36948	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11621	24216	37541	3.08	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11621	24218	37542	3.08	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944	24499		3.5	5.4E-01	A1858398.1	EST_HUMAN	w137g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
503	13287	25921	1.54	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2136	14866	27596	1.01	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2136	14866	27597	1.01	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2789	15491	28230	6.83	5.3E-01	4506323	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

Page 49 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	16491	28231	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSCCL) gene, complete cds
4187	16928		1.58	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30860	1.96	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30861	1.96	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711 5'
5468	18285	31156	0.84	5.3E-01	AA183872.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5468	18265	31157	0.84	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5559	18358	31266	1.82	5.3E-01	BE045620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5559	18358	31287	1.82	5.3E-01	BE045620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8802	21494		1.8	5.3E-01	L01860.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8854	21545	34692	0.91	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
8854	21545	34693	0.91	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
10111	22759	35671	0.62	5.3E-01	A1954210.1	EST_HUMAN	w94b02.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
11650	24149	37460	7.3	5.3E-01	BE566291.1	EST_HUMAN	601339867F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3682168 5'
11789	24379	37709	1.72	5.3E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
11877	25208		4.03	5.3E-01	AA916053.1	EST_HUMAN	cg30a05.s1 NCL_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
797	13569	26229	18.35	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1141	13898	26557	8.29	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1169	13923	26585	1.77	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1879	14616		2.35	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2142	14872	27605	2.55	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3117	15882	28521	1.23	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S26/3 POMF81A and POMF90A precursor, genes, complete cds
3231	15994		1	5.2E-01	ID73443.1	NT	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3400	16158		1.58	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3437	16193	28543	2.27	5.2E-01	AA984165.1	EST_HUMAN	ant7g05.s1 Stratiogene schizobrain S11 Homo sapiens cDNA clone IMAGE:1018504 3'

Page 50 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16376		0.76	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding
4568	17303	26930	0.82	5.2E-01	6752947	NT	chloroplast protein, complete cds
4953	17678		1.02	5.2E-01	7106444	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5567	18364	31272	0.87	5.2E-01	AA284261.1	EST_HUMAN	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
9630	25126	35474	0.75	5.2E-01	X02218.1	NT	zc44409.17 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325189 3'
9630	25126	35476	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832	22483	35685	0.48	5.2E-01	AA194518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9926	22574	35772	1.35	5.2E-01	AF143952.2	NT	zq05009.11 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:628793 5'
12744	25010		7	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
603	13381	26013	1.84	5.1E-01	M58509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
633	13412	26047	4.49	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
633	13412	26048	4.49	5.1E-01	AJ233944.1	NT	Polyglutamine vitellinum (strain PI vt1) 16S rRNA gene
1648	14394		1.09	5.1E-01	X87885.1	NT	Polyglutamine vitellinum (strain PI vt1) 16S rRNA gene
2017	14762		1.29	6.1E-01	BF683096.1	EST_HUMAN	R. norvegicus mRNA for mammalian fusca protein
4057	16902	29433	3.86	5.1E-01	A189495.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288117 5'
4164	16904	29533	2.81	5.1E-01	P96380	SWISSPROT	w198b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
6103	17821	30438	1.01	6.1E-01	U72653.1	NT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6128	18908	31874	0.67	5.1E-01	BE541068.1	EST_HUMAN	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6183	18980		0.93	5.1E-01	AV712326.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6318	19479	32502	1.69	6.1E-01	R80873.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAALF07 5'
8470	21162	34304	0.63	5.1E-01	AW806881.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34305	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9583	22238	35420	4.33	6.1E-01	J05412.1	NT	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9587	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	Human regenerating protein (reg) gene, complete cds
10060	22708	35926	0.89	5.1E-01	M94578.1	NT	66B1 Human retina cDNA Tap509-cleaved sublibrary Homo sapiens cDNA not directional
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	Human carboxyl ester lipase (CEL) gene, complete cds
12328	24745		3.55	5.1E-01	BF439982.1	EST_HUMAN	601566863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
2130	14861	27590	1.24	5.0E-01	4885552	NT	nac51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2130	14861	27591	1.24	5.0E-01	4885552	NT	TAR1 repetitive element ;
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA

Page 51 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27601	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2140	14870	27602	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3811	16583	28198	1.13	5.0E-01	L38483.1	NT	Rattus norvegicus legged protein mRNA, complete cds
3884	16604	28241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	18312		0.65	5.0E-01	BF576189.1	EST_HUMAN	602132842F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4271839 5'
7582	20232	33334	0.75	5.0E-01	AL181549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7582	20232	33335	0.75	5.0E-01	AL181549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
8428	21121		1.92	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8569	21261	34399	0.71	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9388	20429	33547	2.74	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9525	22178	35362	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	35363	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10290	22838		1.12	5.0E-01	BE669218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12026	24554		4	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24989		1.88	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12726	24997		4.39	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
772	13544	26205	2.43	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1656	14402	27090	1.54	4.9E-01	AJ243855.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1899	14638	27345	1.15	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5321	18124	30783	0.89	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31688	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7352	20033	33111	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHAN-ACETYLGLUCOSAMINYLTRANSFERASE
7605	20271	33379	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHAN-ACETYLGLUCOSAMINYLTRANSFERASE
8888	21579		1.45	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4102503 5'

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8088	21775	34939	0.99	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807266 3' similar to TR:086714
9198	26431		1.96	4.9E-01	10946863	NT	Q95714 HERC2.1
10216	22884	36076	0.84	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10419	23085	36286	0.77	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
11925	24486		1.72	4.9E-01	AF176912.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
12709	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
							nc22e11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:114662 3'
4288	17037		0.77	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5420	18219	30930	10.78	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6579	19342	32358	0.79	4.8E-01	J02982.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6589	19352		3.76	4.8E-01	AA659878.1	EST_HUMAN	mus85f09.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7216	19901		1.99	4.8E-01	5031950	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7585	20235	33339	0.78	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7681	20325	33434	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7691	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33621	1.2	4.8E-01	AI820744.1	EST_HUMAN	M77f10.y5 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MIER8 repetitive element
9144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
10629	23322		1.88	4.8E-01	X83502.1	NT	S. cerevisiae ORFs from chromosome X
12217	25165		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
12705	25216		1.66	4.8E-01	AI132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6422	19190	32188	8.41	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086387 5'
6941	19423	32438	0.94	4.7E-01	AI204374.1	EST_HUMAN	q7/2a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7764	20460	33584	0.93	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
7784	20460	33585	0.89	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8974	21664	34816	0.52	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10751	23436		6.11	4.7E-01	AF102873.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11022	23694	36957	2.2	4.7E-01	U41069.1	NT	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 18, and partial cds
11252	23914	37208	1.61	4.7E-01	BF529658.1	EST_HUMAN	602043889F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
11349	24039	37342	1.7	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12118	24609		1.52	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12237	24689		1.51	4.7E-01	AW341591.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809188 3'

Page 53 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12813	25055		1.63	4.7E-01	AP000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt, position (777)
12817	25300		1.38	4.7E-01	6678902	NT	Mus musculus proteasome (prosome, macropain) 26S subunit, ATPase 3 (Pamc3), mRNA
3728	16479	29116	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3726	16479	29117	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18138	30785	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5333	18138	30786	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5385	18185	30875	3.11	4.6E-01	Q90943	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5385	18185	30876	3.11	4.6E-01	Q90943	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
6459	18258	31148	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5472	18271	31163	2.17	4.6E-01	A1247679.1	EST_HUMAN	qt59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5472	18271	31164	2.17	4.6E-01	A1247679.1	EST_HUMAN	TR:O15338 O15338 BUTYROPHILIN.;
5480	18278	31175	1.8	4.6E-01	P20050	SWISSPROT	qt59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5560	18357		0.98	4.6E-01	AF212124.1	NT	MEIOSIS SPECIFIC PROTEIN HOP1
5645	18440		0.77	4.6E-01	BE817247.1	EST_HUMAN	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5809	18598	31526	0.59	4.6E-01	D26215.1	NT	PMD-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6163	18940	31811	1.21	4.6E-01	AE000894.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6659	19586	32620	3.2	4.6E-01	U62332.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6659	19586	32620	3.2	4.6E-01	U62332.1	NT	Emeritella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6659	19586	32621	3.2	4.6E-01	U62332.1	NT	Emeritella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	23105	32884	0.57	4.6E-01	L07320.1	NT	Emeritella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7629	20295	33403	0.91	4.6E-01	AA493577.1	EST_HUMAN	Murine cytomegalovirus e1 protein gene, complete cds
							rh04h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843353 similar to contains Alu repetitive element; contains element L1 repetitive element;
							GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT
7658	20322		0.59	4.6E-01	Q90069	SWISSPROT	PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN A
8219	20913	34049	10.11	4.6E-01	BF697399.1	EST_HUMAN	(C1); 8 KD PROTEIN 2 (8K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI>
							602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4267828 5'
9201	21870	35035	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL Natriuretic Peptide Receptor B Precursor (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

Single Exon Probes Expressed in Brain

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9201	21870	35038	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL Natriuretic Peptide Receptor B Precursor (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9878	22528	35720	1.64	4.6E-01	A1815634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9878	22528	35721	1.64	4.6E-01	A1815634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10912	23592		2.3	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10922	23602	36850	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10922	23602	36851	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	38449	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	38450	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24845		1.77	4.6E-01	D53318.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03
1904	14641	27350	1.43	4.5E-01	AE001831.1	NT	5'
1904	14641	27351	1.43	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2873	15640	28284	4.5	4.5E-01	AA677088.1	EST_HUMAN	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
3312	16072	28722	4.58	4.5E-01	Q05783	SWISSPROT	zif5d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454178 3'
3372	16131	28787	1.07	4.5E-01	AF126378.1	NT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
4007	18753		0.95	4.5E-01	Q28247	SWISSPROT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4055	16800	29431	0.88	4.5E-01	A1708908.1	EST_HUMAN	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4155	17887		4.25	4.5E-01	AW973495.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4890	17617	30236	1.1	4.5E-01	BE963445.2	EST_HUMAN	ss96e08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
5461	18260	31151	1.49	4.5E-01	AW608814.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
6510	19275		1.46	4.5E-01	Q00958	SWISSPROT	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868023 3'
7312	19995	33073	1.27	4.5E-01	M37036.1	NT	QV2-P10012-140100-031-c09 P10012 Homo sapiens cDNA
7509	20180	33273	2.54	4.5E-01	A1868849.1	EST_HUMAN	COAT PROTEIN
7621	20287	33388	0.85	4.5E-01	P50070	SWISSPROT	Rat nuclear proteins B23.1 and B23.2
8206	20900		0.86	4.5E-01	M32661.1	NT	w32e02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8302	20986	34134	3.5	4.5E-01	A1848566.1	EST_HUMAN	SWISNF COMPLEX 170 KDA SUBUNIT ; DNA PRIMASE D melanogaster Shaw2 protein mRNA, complete cds
							ts56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8457	21149	34292	0.83	4.5E-01	Q52728	SWISSPROT	Homo sapiens hypothetical protein DKFZp47G183 (DKFZp47G183), mRNA
8680	21372		2.34	4.5E-01	11444786	NT	

Page 55 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8997	21688	34728	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9940	22491		1.02	4.5E-01	9630816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
10392	23038	36255	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
10772	23455	36899	2.15	4.5E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCL CGAP_U18 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11217	23880		1.52	4.5E-01	AV718382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1] ;
11895	25384		3.52	4.5E-01	BE971461.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLOCED12 5'
12640	24880		1.58	4.5E-01	BF337531.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12811	24918		3.37	4.5E-01	11422009	NT	602035275F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183290 5'
2388	15109	27847	3.39	4.4E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3310	16070	28719	1.29	4.4E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	16070	28720	1.29	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3313	16073	28723	2.92	4.4E-01	BF056728.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4209	16950		1.88	4.4E-01	BE378707.1	EST_HUMAN	791d02.y1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
5334	18137	30797	1.2	4.4E-01	P04929	SWISSPROT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5334	18137	30798	1.2	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5602	18397	31309	1.59	4.4E-01	S65019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5819	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5864	18651	31591	1.46	4.4E-01	AI188413.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLOCSC12 5'
5864	18651	31592	1.46	4.4E-01	AI188413.1	EST_HUMAN	q62h11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6146	18923	31894	1.78	4.4E-01	AW080795.1	EST_HUMAN	q62h11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6236	19010		1.42	4.4E-01	AA776132.1	EST_HUMAN	xc27e09.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685510 3' similar to TR:Q95154 Q95154
7287	19980	33056	1.04	4.4E-01	AE000571.1	EST_HUMAN	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7723	25119		0.6	4.4E-01	AE001188.1	NT	ae8b611.s1 Strategene solhizo brain S11 Homo sapiens cDNA clone IMAGE:970865 3' similar to gb:M16038
7740	20436		9.71	4.4E-01	Z11679.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8661	21353	34500	0.84	4.4E-01	AA056427.1	EST_HUMAN	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8049	21738	34898	0.7	4.4E-01	AF112540.1	NT	Treponema pallidum section 4 of 87 of the complete genome
							S. tuberosum mRNA for induced stolon tip protein (partial)
							Z169a03.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
							HIV-1 isolate 0810746 from USA, envelope glycoprotein (env) gene, partial cds

Page 56 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21771	34934	0.57	4.4E-01	AW012578.1	EST_HUMAN	hh05c08.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2954222 3' similar to
9180	21860	35025	1.24	4.4E-01	O62836	SWISSPROT	SW-MSH0 HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH0 ;
9862	22612	35709	2.19	4.4E-01	AI268650.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
9883	22613		1.88	4.4E-01	P28922	SWISSPROT	qc39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9997	22645	35857	4.31	4.4E-01	P35590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10273	22921	36132	1.33	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36133	1.33	4.4E-01	S76404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12148	24635	31085	3.44	4.4E-01		NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12679	24803	31000	3.35	4.4E-01		NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12683	24971		1.91	4.4E-01	P54725	SWISSPROT	Autographa californica nucleopolyhedrovirus, complete genome
12766	25152		1.43	4.4E-01	AW363338.1	EST_HUMAN	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
402	13187	25835	2.17	4.3E-01	AF155218.1	NT	RC2-CT0320-281199-012-c07 CT0320 Homo sapiens cDNA
402	13187	25836	2.17	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2876	15642		1.64	4.3E-01	AW935269.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3056	15822	28468	0.75	4.3E-01	AW999477.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4131	16873	29501	1.29	4.3E-01	J00308.1	NT	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4374	13187	25835	1.18	4.3E-01	AF155218.1	NT	Human somatostatin 1 gene and flanks
4374	13187	25836	1.18	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4902	17629		1.19	4.3E-01	AL161502.2	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5280	18085	30742	0.8	4.3E-01	P48634	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5280	18085	30743	0.8	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5798	18589	31515	1.59	4.3E-01	BE181655.1	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5817	18606	31534	2.02	4.3E-01	AF178925.1	NT	QV1-HT0838-070500-191-d08 HT0838 Homo sapiens cDNA
6008	18371	32384	4.78	4.3E-01	AJ001878.1	NT	Salmonella typhimurium flagellin gene, partial cds
6689	19608	32648	0.6	4.3E-01	AF075629.1	NT	Coturnix coturnix japonica lfnG gene
6767	19511		0.91	4.3E-01	O33367	SWISSPROT	Equus caballus microsatellite LEX027
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	DNA GYRASE SUBUNIT B
7498	20168	33260	0.61	4.3E-01	U51002.1	NT	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4168298 5'
8326	21019		2.72	4.3E-01	U97040.1	NT	Mus musculus Dlx-2 gene, complete cds
9154	21885	35053	0.96	4.3E-01	Y14604.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
9626	22279	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	Ervnlia amylovora rcsV gene
9626	22279	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
							hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	22776	35990	0.84	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10409	23055	36272	0.5	4.3E-01	H65292.1	EST_HUMAN	TR:O00189 O00189 NU-ADAPTIN-RELATED PROTEIN 2 ;
10849	19608	32846	2.45	4.3E-01	AF075629.1	NT	yr45b05.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:208209 3'
11166	23833	37113	1.29	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11166	23833	37114	1.29	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
11745	24336	37862	1.84	4.3E-01	AI874332.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
12770	28029		2.18	4.3E-01	AJ003022.1	NT	h84d04.x1 NCL_CGAP_OY65 Homo sapiens cDNA clone IMAGE:2283351 3'
1337	15568	26761	1.64	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor wihH gene
1941	14878		1.23	4.2E-01	AA761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3598	16349	28990	4.4	4.2E-01	AE003947.1	NT	nz24a09.s1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:1286698 3'
3628	16381	28021	1.41	4.2E-01	AI280338.1	EST_HUMAN	Xylella fastidiosa, section 93 of 229 of the complete genome
3698	17888		0.85	4.2E-01	N81203.1	EST_HUMAN	q194b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876945 3'
3964	16713	28352	0.87	4.2E-01	Q04886	SWISSPROT	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07878, Z40488
4649	17383	30015	4.88	4.2E-01	AA534093.1	EST_HUMAN	SOX-8 PROTEIN
4731	17463	30100	3.46	4.2E-01	R13467.1	EST_HUMAN	h99h01.s1 NCL_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5628	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	yf77e01.t1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5693	18487	31408	1.63	4.2E-01	AW854162.1	EST_HUMAN	601879/21F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
6112	18889	31858	1.01	4.2E-01	AL163247.2	NT	RC3-CT0264-080400-028-g04 CT0264 Homo sapiens cDNA
6852	19552	32582	10.8	4.2E-01	AU158472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6852	19552	32583	10.8	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6911	26101	32994	2.15	4.2E-01	S82504.1	NT	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6983	19686	32734	7	4.2E-01	AL161647.2	NT	Brcal-breast cancer gene [rats, W.F. spleen, Genomic, 419 nt, segment 2 of 2]
7891	20586	33715	2.21	4.2E-01	AW957448.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7891	20586	33716	2.21	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8108	20800	33932	0.61	4.2E-01	4758039	NT	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8870	22620		0.94	4.2E-01	AA705007.1	EST_HUMAN	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10081	22729	35944	0.45	4.2E-01	AF181894.1	NT	z195f01.s1 Soares fetal liver spleen 1N1FLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10393	23039	36256	1.78	4.2E-01	AW863666.1	EST_HUMAN	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10972	23648	36901	2.69	4.2E-01	AB023489.1	NT	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11370	23977	37277	2.11	4.2E-01	BE968485.2	EST_HUMAN	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
1072	13830	26488	1.83	4.1E-01	AI905481.1	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
							RC-BT091-210199-142 BT091 Homo sapiens cDNA

Page 58 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13839	28497	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1081	13839	28488	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2716	16422	28161	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2941	15706	28355	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2941	15706	28356	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16506	29142	0.68	4.1E-01	AW981292.1	EST_HUMAN	EST373384 MAGE resequences, MAGG Homo sapiens cDNA
3754	16506	29143	0.68	4.1E-01	AW981292.1	EST_HUMAN	EST373384 MAGE resequences, MAGG Homo sapiens cDNA
4241	16982	28607	2.93	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4271	17011		0.82	4.1E-01	AA909257.1	EST_HUMAN	om33402 s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1642819 3'
4618	17363	29988	1.48	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
4888	18057	28706	2.48	4.1E-01	AA806344.1	EST_HUMAN	q94b08 s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
5899	18684	31632	4.72	4.1E-01	BF681393.1	EST_HUMAN	602166590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287319 5'
7332	20014	33092	2.78	4.1E-01	U67635.1	NT	Methanococcus jannaschii section 77 of 160 of the complete genome
7835	20630	33757	1.38	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
8888	21678	34827	1.39	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpac-pending), mRNA
9465	22075		0.67	4.1E-01	AF160597.1	NT	Voelavo gymnocauidus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10163	22811		1.05	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 3/6
10310	22857	36173	0.91	4.1E-01	AV849579.1	EST_HUMAN	AV849579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10404	23050	36267	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10404	23050	36268	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10478	23124		1.33	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
10743	23430	36673	80.48	4.1E-01	X58700.1	NT	Zea mays ZMFW52 gene for 19 kDa zein protein
11368	23177	38404	2	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1)(HBK1)
12476	25860		2.82	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1016	13775	26435	0.82	4.0E-01	8404656	NT	Leaqueus rubellus mitochondrion, complete genome
1316	14065	26739	0.95	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1468	14215		4.05	4.0E-01	6879268	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1999	15683	27457	1.16	4.0E-01	Z96933.1	NT	Ascobolus immerus mas2 gene
1999	15683	27458	1.16	4.0E-01	Z96933.1	NT	Ascobolus immerus mas2 gene
2168	14886	27619	1.19	4.0E-01	AE001931.1	NT	Delnocooccus radiodurans R1 section 68 of 229 of the complete chromosome 1
2158	14886	27620	1.19	4.0E-01	AE001931.1	NT	Delnocooccus radiodurans R1 section 68 of 229 of the complete chromosome 1
2808	12852	25595	1.4	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recoglin (Ubr1), mRNA

Page 59 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2668	15734	28383	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2668	15734	28384	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3683	16436	29080	1.98	4.0E-01	AF008690.1	NT	Streptococcus pneumoniae Y1C (y1C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3607	16559	29191	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3607	16559	29192	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4767	17499	31849	7.97	4.0E-01	Q31849	SWISSPROT	NADH+PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5820	18609	31538	1.23	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6345	19115	32104	0.94	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7728	20391	33504	0.86	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7829	20524	33649	0.44	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-18080-202-g02 TN0110 Homo sapiens cDNA
7910	20605	33736	1.04	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8804	21595	34738	1.17	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030262.1	EST_HUMAN	601568283F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3828092 5'
11721	24315		2.83	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12162	25222		2.26	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12684	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1356	14104	26780	1.85	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2648	15358	28101	3.34	3.9E-01	AB033018.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2709	15418	28153	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2709	15418	28154	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3093	15858	28499	4.73	3.9E-01	AJ225896.1	NT	Shorhizobium meliloti egl, syrB2, cys3 genes and orf3
4059	16804	29435	1.05	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCI_CGAP_B118 Homo sapiens cDNA clone IMAGE:3339189 3'
4932	17660	30270	1.74	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3833699 5'
5943	18631	31568	3.91	3.9E-01	BF208038.1	EST_HUMAN	601862362F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4082055 5'
7554	20549	33674	0.92	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT1016-170899-004-b08 CT10105 Homo sapiens cDNA
8769	21461		0.59	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9134	21822	34988	1.26	3.9E-01	AW195688.1	EST_HUMAN	xt86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821
9445	22122	35301	1.46	3.9E-01	AI937337.1	EST_HUMAN	SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22429	35636	3.03	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
9846	22498		0.98	3.9E-01	11485620	NT	Porphyra purpurea mitochondrion, complete genome
10068	22714	35932	0.77	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCQC11 5'
11763	24344	37674	1.47	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBDBE08 5'
11948	26295		3.37	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12066	24581		2.08	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10593 (FLJ10593), mRNA
158	12971		8.33	3.8E-01	7079488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1863	14601		1.03	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 226 of the complete genome
2460	15178	27918	1.29	3.8E-01	U41948.1	NT	Ceanorhabditis briggsae acetylcholinesterase (ace-1) gene, complete cds
2678	15280	28027	1.62	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2838	15601	28092	3.96	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	15769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 89SE-MP1213)
3043	15809	28456	1.39	3.8E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3477	16233	28887	7.98	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3841	16283		1.22	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16492	29127	1.16	3.8E-01	BE164080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16647	29287	0.97	3.8E-01	6754095	NT	Mus musculus general transcription factor II (Gt2), mRNA
4043	16788	29416	0.74	3.8E-01	AJ271361.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	18021		0.74	3.8E-01	S46825.1	NT	p10n protein [mink, Genomic, 2448 nt]
6528	19294	32288	5.6	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-602 BT0537 Homo sapiens cDNA
6862	19579	32614	4.58	3.8E-01	AI374601.1	EST_HUMAN	la54f11.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
7418	20093		4.42	3.8E-01	X61597.1	NT	M. musculus gene for kallikrein-binding protein
8196	20890	34028	0.86	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8455	21147	34289	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KAA1631 protein, partial cds
8523	21215	34358	1.02	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8718	21408	34551	1.28	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.65	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120639 5' similar to contains Alu repetitive element; contains PTRs repetitive element;

Page 61 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10895	23386		1.67	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11921	24121		3.18	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-012 HT0841 Homo sapiens cDNA
11693	24288	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11693	24288	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12149	24636		4.76	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12270	25318		2.08	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12384	24779		3.39	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-e05 ET0063 Homo sapiens cDNA
12723	24984		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
12771	25291		1.74	3.8E-01	AF281483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
12788	25040	30969	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27944	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3453	18209	28860	9.64	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	29572	7.39	3.7E-01	AI218707.1	EST_HUMAN	dk39c07.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4286	17025	29651	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-002 OT0007 Homo sapiens cDNA
4357	17085	29730	2.65	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
5678	18470	31388	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5860	18647	31588	0.8	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8417	19185	32183	0.86	3.7E-01	MT0806.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
6438	19204		0.72	3.7E-01	L10353.1	NT	Mus saxicola haptoglobin mRNA, complete cds
7043	19734	32784	3.23	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA
7685	20349	33463	0.6	3.7E-01	T68802.1	EST_HUMAN	ye50a07.3 Soares fetal liver spleen 1N1L3 Homo sapiens cDNA clone IMAGE:66324 5'
7719	20383	33497	0.55	3.7E-01	AW511328.1	EST_HUMAN	hd46a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element/contains L1, L2, L1 repetitive element
8227	20921	34059	2.07	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
8263	20957	34098	0.65	3.7E-01	AA902912.1	EST_HUMAN	dk43b11.s1 NCL_CGAP_Lel2 Homo sapiens cDNA clone IMAGE:1616701 3'
9101	21789		1.31	3.7E-01	AJ271388.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10089	22717		0.6	3.7E-01	K06891.1	NT	mouse Ig germline alpha membrane exons region
10110	22758	35970	4.12	3.7E-01	AJ338411.1	EST_HUMAN	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950897 3'
10764	23448	36890	1.98	3.7E-01	X05959.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHG)
10957	23633	36882	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIND1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIND1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11676	24271	37593	1.43	3.7E-01	D76848.1	EST_HUMAN	HUM230A06B Human aorta polyA+ (TFJujwara) Homo sapiens cDNA clone GEN-230A08 5'

Page 62 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11771	24362		2.87	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11889	24943		2.11	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24558		3.09	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12488	24847		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
12548	24888	30895	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
254	13062	25701	2.17	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
976	13740		8.22	3.6E-01	U69241.1	NT	Human mlbp gene, partial cds
1291	14040	28713	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1291	14040	26714	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1909	14846	27356	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1909	14846	27357	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1944	14679	27393	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2267	14893		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.89	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2479	15197	27938	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27937	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27950	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2636	15348	28090	1.44	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2900	17884		7.16	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3462	16218	28871	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3462	16218	28872	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4375	17112	29745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4948	17675	30285	2.38	3.6E-01	AW339393.1	EST_HUMAN	he02g04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5288	18103	30782	0.82	3.6E-01	AJ006869.1	NT	Homo sapiens lipo gene Intron 5
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6386	19155	32154	1.74	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7048	19739		3.2	3.6E-01	R94090.1	EST_HUMAN	yt74a06.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:275987 5'
7183	19869	32943	1.9	3.6E-01	AW021714.1	EST_HUMAN	w72c10.x1 Soares thymus NHFFth Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8123	20817	33953	0.59	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1]; SCO-SPONDIN

Page 63 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8800	21591	34731	2.74	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091	21780	34944	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9299	21966	35139	1.04	3.6E-01	X17550.1	NT	D. melanogaster slinged gene, exons 3, 4, 5 & 6
9299	21966	35140	1.04	3.6E-01	X17550.1	NT	D. melanogaster slinged gene, exons 3, 4, 5 & 6
9369	21944		0.57	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
9763	22414	35621	14.67	3.6E-01	Q63194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893	22543	35735	0.61	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.61	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10884	23544	36791	3.31	3.6E-01	BE802390.1	EST_HUMAN	601876418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11062	23722	36983	4.12	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11421	23188	36419	3.4	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11903	25415		1.83	3.6E-01	Y19210.1	NT	Homo sapiens h-hb5 gene for hair keratin, exons 1 to 9
11978	24522		1.4	3.6E-01	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
12135	24624		4	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12493	24850		2.12	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 10 (AF10), mRNA
12746	25363		2.23	3.6E-01	AW190229.1	EST_HUMAN	x60et1.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00588 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.69	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
708	13482	26132	1.59	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
782	13535	26194	4.25	3.5E-01	BF129798.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615	14362	27063	1.1	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4124244 5'
1636	14382	27069	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E-01	P06798	SWISSPROT	HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2812	15600	28086	1.76	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'

Page 64 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16637		0.85	3.5E-01	AA642138.1	EST_HUMAN	nt60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA IMAGE:1172357 3'
4231	16972	29596	1.67	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
4443	17179	29805	0.94	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4627	17362	29995	1.02	3.5E-01	Y18477.1	NT	Mus musculus Alex12B gene 5' flanking region
4880	17607	30230	4.59	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5251	18057	30885	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30886	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5462	18281	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6143	18921		0.98	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.6	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.r1 Soares_testis_NHT Homo sapiens cDNA IMAGE:782429 5' similar to TR:G1066935
6359	19129	32124	0.68	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6568	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6956	19438		4.24	3.5E-01	X98505.1	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7970	20665		2.19	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7973	20688	33780	0.71	3.5E-01	BF388871.1	EST_HUMAN	RC4-ET0024-260600-014-c07 ET0024 Homo sapiens cDNA
8368	21059		0.63	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8825	21517	34662	1.17	3.5E-01	4507810	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9636	22288	35481	1.62	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9786	22437	35844	5.84	3.5E-01	Z28825.1	NT	X. laevis gene for albumin including HP1 enhancer
9867	22517	35713	0.96	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10635	23327	36564	2.78	3.5E-01	X61084.1	NT	C. griseus rhodopsin gene for opsin protein
10948	23625	36675	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10948	23625	36676	2.38	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24106	37419	1.34	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11585	24184	37499	1.64	3.5E-01	N07759.1	EST_HUMAN	yz90h12.r1 Soares_multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:290375 5'
11619	24216		1.71	3.5E-01	M82865.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11684	24279	37601	1.51	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
11776	24387		1.36	3.5E-01	A1064773.1	EST_HUMAN	HA0542 Human fetal liver cDNA library Homo sapiens cDNA
12063	24578		1.47	3.5E-01	X84585.1	NT	B. taurus alpA1 gene for F0(F-1) ATP synthase alpha-subunit
12214	24676		2.32	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.5E-01	AE001691.1	NT	<i>Thermoboga maritima</i> section 3 of 138 of the complete genome
12783	26289	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12793	26269	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	13466		1.85	3.4E-01	AL242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
955	13720	26388	7.61	3.4E-01	Y09798.2	NT	<i>Pseudomonas fluorescens</i> colR, ccdS genes, orf222 and partial inaA gene
1303	14052	28726	1.72	3.4E-01	Y00554.1	NT	<i>Azotobacter vinelandii</i> nifA gene for NifA protein (positive regulatory element)
2400	15121	27858	2.62	3.4E-01	D90909.1	NT	<i>Synechocystis</i> sp. PCC6803 complete genome, 11/27, 1311235-1430418
3001	15787	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15787	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3146	15910	28555	1.08	3.4E-01	D90909.1	NT	<i>Synechocystis</i> sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28568	6.23	3.4E-01	U83905.1	NT	<i>Canis familiaris</i> rod photoreceptor cGMP-gated channel alpha-subunit (CNGB1) mRNA, complete cds
3338	16098	28749	0.9	3.4E-01	AF034892.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28933	3.48	3.4E-01	AF108835.1	NT	<i>Methylovorus</i> sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.69	3.4E-01	BF449010.1	EST_HUMAN	7n94e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15 Q8UJ15 DJ18C9.1
4029	16774		2.38	3.4E-01	AA584198.1	EST_HUMAN	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4460	17196	29823	0.82	3.4E-01	AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4599	17334	28983	1.54	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4898	17625		3.23	3.4E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5143	17862		0.98	3.4E-01	U79746.1	NT	Homo sapiens serotonin transporter (hSERT) gene, promoter region, exons 1B and 2, and partial cds
5599	18394	31304	2.62	3.4E-01	AL161594.2	NT	<i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 90
6721	18613		6.09	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.e1 Stratagene hNT neuron (#837293) Homo sapiens cDNA clone IMAGE:547221 3'
5917	18702		1.99	3.4E-01	L02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5940	18722	31681	0.88	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	UI-HB11-aet-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249.t1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A249 5'
6844	19406		1.66	3.4E-01	N95225.1	EST_HUMAN	zb59e12.s1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:307342 3'

Page 66 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6948	19548	32578	1.02	3.4E-01	AI468082.1	EST_HUMAN	hm63q05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
6959	19441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7806	20501		0.49	3.4E-01	AE000493.1	NT	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8135	20829	33984	0.0	3.4E-01	Y14930.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
							Homo sapiens TCRAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF448010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
8366	21078		1.51	3.4E-01	AA337063.1	EST_HUMAN	Q9UJ16 DJ18C9.1;
8461	21153	34296	0.72	3.4E-01	LO4690.1	NT	EST141765 Endometrial tumor Homo sapiens cDNA 5' end
8751	21443	34560	1.7	3.4E-01	9833824	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9112	21800	34964	4.42	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9112	21800	34965	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9321	21988		0.51	3.4E-01	AB017610.1	NT	INTEGRIN BETA-8 PRECURSOR
9346	20417	33536	4.67	3.4E-01	U19492.1	NT	Ephedra fluviatilis mRNA for PLC-gamma8, complete cds
9397	22059	35229	0.5	3.4E-01	AF163887.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9595	22248	35433	1.01	3.4E-01	U68763.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9789	22440	35848	1.86	3.4E-01	AJ225084.1	NT	Dicystosellum discoideum putative CMF receptor CMFR1 mRNA, complete cds
10376	23022		0.62	3.4E-01	AE004098.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
10940	23620		4.72	3.4E-01	AE000881.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10984	23659	36912	2.6	3.4E-01	P06925	SWISSPROT	Vibrio cholerae chromosome I, section 4 of 261 of the complete chromosome
11032	23703	36971	2.17	3.4E-01	AF045981.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
11253	23915	37207	1.81	3.4E-01	M25886.1	NT	PROBABLE E4 PROTEIN
11253	23915	37208	1.81	3.4E-01	M25886.1	NT	Ruizus arceus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11483	24084	37396	1.88	3.4E-01	AB035507.1	NT	Human von Willebrand factor gene, exons 36 and 37
11513	24113	37423	3.65	3.4E-01	AL161515.2	NT	Human von Willebrand factor gene, exons 36 and 37
11788	24376	37706	1.72	3.4E-01	BF061948.1	EST_HUMAN	Rattus norvegicus mRNA for s-glycerinMUC18, complete cds
11861	24445	37786	1.58	3.4E-01	U07000.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11881	24453		1.85	3.4E-01	U93604.1	NT	7k6a012.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480846 3'
12197	24666		11.43	3.4E-01	L26339.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12224	25192		1.61	3.4E-01	BE218652.1	EST_HUMAN	Citrus variegation virus putative replicase gene, partial cds
							Human autoantigen mRNA, complete cds
							hm42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
							PTR5 repetitive element;

Page 67 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25282		2.28	3.4E-01	8838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24781	31038	2.2	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12888	24874		1.82	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
103	12840	25453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
435	13221	25867	0.9	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
618	13397	26032	2.01	3.3E-01	7682485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26697	2.85	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	26705	3.76	3.3E-01	BF58880.1	EST_HUMAN	602184018T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1336	14085	26760	1.2	3.3E-01	U43826.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1601	14347	27038	1.47	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST136722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2404	15125		4.82	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (cotlate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2949	15715	28368	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3051	15817	28462	1.48	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3486	16243	28899	1.07	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3789	16541	28176	2.1	3.3E-01	O84845	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3789	16551	29183	0.97	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3)
3932	16682	29323	1.03	3.3E-01	4757739	NT	Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA
3947	16697	29338	1.47	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3983	16731	29365	1.79	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4334	17073		1.6	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4841	17375		1.23	3.3E-01	AI539114.1	EST_HUMAN	bp78b12.x1 NCL CGAP U13 Homo sapiens cDNA clone IMAGE:2206407 3' similar to gb:X57522 ANTIGEN
4788	17517	30139	1.22	3.3E-01	D64003.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
6148	17865		0.96	3.3E-01	AW637982.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868768
5241	18047	30975	2.61	3.3E-01	X89819.1	NT	QV0-DT0047-170200-123-h08 DT0047 Homo sapiens cDNA
5241	18047	30976	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5241	18047	30976	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein

Page 68 of 536  
Table 4

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5700	18494	31417	0.74	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
5858	18643	31882	1.9	3.3E-01	BE616650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5858	18643	31883	1.9	3.3E-01	BE616650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5947	18729	31888	1.18	3.3E-01	P05691	SWISSPROT	CIRCUINSPOROZOITE PROTEIN (CS)
6695	18612	32851	0.71	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6695	18612	32852	0.71	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6789	19533	32560	4.82	3.3E-01	AI628131.1	EST_HUMAN	ty44h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6789	19533	32561	4.82	3.3E-01	AI628131.1	EST_HUMAN	ty44h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7682	20346	33458	1.88	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460	21152	34295	18.82	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8659	21351	34497	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351	34498	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9012	21702	34852	0.81	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9278	22032	35203	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9411	22073	35244	2.82	3.3E-01	N69868.1	EST_HUMAN	za87h01.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9452	22002	35174	2.77	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9891	22541		2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG(G)-C) gene, exons 1-3, complete cds
10822	23315	36554	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10822	23315	36555	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10951	23628		1.7	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11198	23861	37147	11.81	3.3E-01	BE216351.1	EST_HUMAN	hV61g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176878 3'
11317	24008	37313	3.23	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (36 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
11719	24313		3.09	3.3E-01	AA808621.1	EST_HUMAN	cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338850 3'
11741	12840	25453	1.87	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
11877	24521	37268	1.71	3.3E-01	6598318	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12876	24987		3.34	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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701	13476		1.43	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13694	26555	27.53	3.2E-01	AF047073.1	NT	Fusarium poae Virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26677	1.36	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1369	14117	26792	5.42	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1767	14509	27210	1.25	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27222	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1777	14519	27223	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1835	14574	27286	1.23	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14887	27821	2.52	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2543	15257		2.01	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2713	15420	28159	1.08	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3594	16347		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4305	17044	28669	0.91	3.2E-01	4759195	NT	Homo sapiens synplekin (SYM) mRNA
4363	17101	28736	1.52	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4484	17200	29828	1.21	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4888	17422		6.7	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4828	17557	30179	1.17	3.2E-01	Q67081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
4965	17690	30299	0.74	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888799 5'
5180	17998	30821	3.26	3.2E-01	BE173984.1	EST_HUMAN	GM0-HT0568-060300-268-f10 HT0569 Homo sapiens cDNA
5888	18655	31598	1.07	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6211	18986	31963	0.9	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6501	19266	32268	0.64	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHTA Homo sapiens cDNA clone FHTAABH01 5'
6634	19396		1.09	3.2E-01	AB000239.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
7756	20451	33575	0.51	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8072	20766	33895	1.48	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8164	20868	33990	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8265	20859	34098	14.41	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8268	20862	34103	13.76	3.2E-01	BF311695.1	EST_HUMAN	601887107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126693 5'
8361	21054		1.38	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

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8398	21091	34228	1.24	3.2E-01	BF246771.1	EST_HUMAN	60185580F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4076827 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	60185580F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4076827 5'
8471	21163	34306	2.65	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8571	21263	34401	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
8665	21656	34807	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8978	21666		2.18	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9048	21737	34894	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10098	22747	35862	0.45	3.2E-01	BE376230.1	EST_HUMAN	h93f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181589 3'
10210	22858		3.41	3.2E-01	AB071399.1	NT	Homo sapiens gene for AF-6, complete cds
10568	23261	36486	3.94	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBDDZ21
12010	25317		3.91	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	25374		1.44	3.2E-01	BE886846.1	EST_HUMAN	601507820F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909632 6'
12524	24871		4.21	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12712	25354	30606	1.75	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3616746 6'
2677	15386	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126061 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	18630		1.29	3.1E-01	AW628036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3170	15933		3.35	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3887	16637	29276	0.8	3.1E-01	AJ251566.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4908	17638	30250	0.73	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5390	18180	30882	9.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1298
5514	18312	31213	0.67	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5524	18322		0.88	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5685	18478	31396	2.11	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R94322.1	EST_HUMAN	yq41f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:188397 5'

Page 71 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8374	18143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
8439	19207	32203	1.01	3.1E-01	AI264458.1	EST_HUMAN	q139d01.x1 NCI_CGAP_C88 Homo sapiens cDNA clone IMAGE:1874889 3'
6583	19346	32360	3.91	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6873	25081	30546	2.41	3.1E-01	BE737392.1	EST_HUMAN	801306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7978	20248	33354	0.77	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	IR45318.1	EST_HUMAN	y946f01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
9802	22463	35855	0.84	3.1E-01	6878322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9887	22615	35818	1.05	3.1E-01	BF696839.1	EST_HUMAN	802124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
9887	22615	35819	1.05	3.1E-01	BF696839.1	EST_HUMAN	802124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10029	22677	35893	1.74	3.1E-01	AI244001.1	EST_HUMAN	q181e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:355700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10201	22849		0.83	3.1E-01	T56325.1	EST_HUMAN	y647h08.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74367 3' similar to c1milar to gb:M01038_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10741	23428	36872	1.26	3.1E-01	BF216117.1	EST_HUMAN	801983592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085814 5'
11524	24124	37430	2.56	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	24623		1.48	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
12165	24647		3.03	3.1E-01	AF304162.1	NT	Sizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12304	24729		2.82	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12680	24860		3.48	3.1E-01	AF196778.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel $\alpha$ )
12699	25347		1.35	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp1-pending), mRNA
70	15512	25533	2.01	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc $\epsilon$ ), mRNA
247	13058	25886	14.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1202	13954	26818	2.51	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1487	14244	26930	6.57	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atlat natriuretic peptide
2132	14862	27592	1.2	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3208	15969		1.18	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyketonate lyase, complete cds
3848	16597	28234	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261189-001-g01 ST0262 Homo sapiens cDNA
4477	17212	28937	1.95	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atlat natriuretic peptide
5287	18073	30702	7.22	3.0E-01	BE741629.1	EST_HUMAN	801594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5349	18152	30833	0.77	3.0E-01	AF229247.1	NT	Canigato orthopoxvirus hemagglutinin gene, complete cds

Page 72 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5417	18218	30924	3.94	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5417	18218	30925	3.94	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 129/ev Clara cell 10 kd protein (mCC10) gene, complete cds
6732	19566	32598	3.06	3.0E-01	D16313.1	NT	Mouse cytokera15 gene, complete cds
6732	17931	30567	0.61	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
6827	19488	32510	0.85	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7021	19713	32770	0.71	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7227	19912	32985	2.77	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PepA (pepA) gene, partial cds
7827	20522	33648	1.3	3.0E-01	AE001755.1	NT	Thermotoga maritima section 97 of 130 of the complete genome
8271	20865		2.97	3.0E-01	8910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (ClactB), mRNA
8374	21067	34207	1.32	3.0E-01	BE560383.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681694 5'
8728	21420	34584	0.51	3.0E-01	AF141878.1	NT	Streptomyces sulfonolactans isopenicillin N synthase (pcbC) gene, partial cds
8770	21462		0.8	3.0E-01	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9118	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9856	22506		43.84	3.0E-01	BE001129.1	EST_HUMAN	RC2-BN0074-240400-110-m12 BN0074 Homo sapiens cDNA
9868	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10042	22690	35908	0.49	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), Tadb (tadb), Tadc (tadc), Tadd (tadd), Tade (tade), Tadf (tadf), and Tdg (tdg) genes, complete cds
10042	22690	35909	0.49	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), Tadb (tadb), Tadc (tadc), Tadd (tadd), Tade (tade), Tadf (tadf), and Tdg (tdg) genes, complete cds
10294	22941	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10298	22943	36157	1.88	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
10316	22963	36179	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10316	22963	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
11772	24363	37694	1.95	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
11772	24363	37695	1.95	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
12416	25302		2.52	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12693	25345		5.51	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
2018	14753	27481	1.43	2.8E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2245	14873	27710	1.16	2.9E-01	AF222718.1	NT	Chrysosporium synuroides mitochondrion, complete genome
3246	16008	28658	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-f12 CT0328 Homo sapiens cDNA

Page 73 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3248	16008	28659	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3877	16627	29265	0.72	2.9E-01	AI610836.1	EST_HUMAN	tp21at11.X1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2189412 3' similar to gb/D15050 NIL-2-A
4062	16787	29427	0.73	2.9E-01	AB016426.1	NT	ZINC FINGER PROTEIN (HUMAN) contains element L1 repetitive element;
4084	16809		0.77	2.9E-01	AW002902.1	EST_HUMAN	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4462	17188	29813	1.1	2.9E-01	AA294468.1	EST_HUMAN	w027f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
5177	17988		1.86	2.9E-01	R37485.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element
5310	19507	32532	0.79	2.9E-01	AF321001.1	NT	y77e12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5877	18471	31387	5.19	2.9E-01	X56098.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5877	18471	31388	5.19	2.9E-01	X56098.1	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansucrase
5889	18482	31401	6.4	2.9E-01	6878982	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levansucrase
5985	18747	31708	1.47	2.9E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
6187	18964	31937	1.08	2.9E-01	AI797129.1	EST_HUMAN	z097b12.r1 Soares NIHMPu.S1 Homo sapiens cDNA clone IMAGE:787711 5'
6233	18007	31984	2.4	2.9E-01	U03420.1	NT	w027e05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.L1 L1 repetitive element;
6365	18135	32130	0.98	2.9E-01	R69194.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6366	19135	32131	0.88	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141616 5'
6621	19383		0.56	2.9E-01	Z50156.1	NT	y39d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141616 5'
6890	17966	30523	1.52	2.9E-01	AF142329.1	NT	D discoidum gene for 34 kD actin binding protein
6898	18688	32737	2.95	2.9E-01	Q04369	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7059	19750	32813			AF100956.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7620	20515	33640	1.87	2.9E-01	BE640422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
7620	20515	33841	1.07	2.9E-01	BE640422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33875	0.48	2.9E-01	AJ237937.1	NT	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33876	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8062	20756		0.94	2.9E-01	BF217743.1	EST_HUMAN	Bos taurus partial stat5A gene, exons 5-19
8237	20831		0.49	2.9E-01	AF197486.1	NT	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
							Buchnera aphidicola plasmid pLeu isolate M1 2-Isopropylmalate synthase (leuA) gene, partial cds; 3-Isopropylmalate dehydrogenase (leuB) gene, complete cds; and Isopropylmalate dehydratase subunit (leuC) gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	21185	34328	0.84	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8923	21515	34980	1.02	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
8931	21622	34765	0.85	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9145	21878	35040	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9145	21878	35041	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
10810	23493	36728	1.93	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37059	1.76	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37060	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.59	2.8E-01	AA95373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element
11578	24178	37493	3.55	2.8E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11600	24199	37519	1.82	2.8E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24199	37520	1.82	2.8E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.8E-01	AF092453.1	NT	Homo sapiens TNF- $\alpha$ -inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.88	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
560	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1061	13819	28481	3.89	2.8E-01	AF168050.1	NT	Gulra gulra oocyte maturation factor Mos (c-mos) gene, partial cds
1254	14003	26871	1.82	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1254	14003	26872	1.82	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1268	14017	26684	1.34	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-085-b05 CT0364 Homo sapiens cDNA
2008	14742	27487	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKFZp588i2321 J1 588 (synonym: huter) Homo sapiens cDNA clone DKFZp588i2321
2127	14858	27588	1.41	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2475	15193	27933	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15193	27934	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2549	15264		1.89	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2670	15380	28118	0.97	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2970	15736		1.29	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2971	15737	28386	2.04	2.8E-01	Z14037.1	NT	B.taurus microsatellite [ETH121]
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B.taurus microsatellite [ETH121]
3373	16132	28788	1.13	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-694000 nt. position (417)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3978	16726	29360	1.69	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4174	16914		1.95	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element contains element MER22 repetitive element;
4422	17158	29789	0.99	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magee9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29783	2.31	2.8E-01	PI13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30128	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4777	17509	30131	2.87	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30182	1.23	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4180128 5'
4829	17580	30182	1.91	2.8E-01	AI272669.1	EST_HUMAN	ql59e11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element contains element L TRS repetitive element;
5228	25084	30880	24.89	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5519	18317	31218	3.07	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
5727	18519		0.95	2.8E-01	AW892683.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
5848	18635		0.63	2.8E-01	AA404576.1	EST_HUMAN	z41101.1 Scores ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6083	25418		0.85	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6632	19394	32409	8.34	2.8E-01	BF511215.1	EST_HUMAN	UI-H-B14-actf04-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7341	20022		1.17	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
7382	20062	33140	0.58	2.8E-01	X63980.1	NT	L. asculentum ypt2 mRNA for GTP-binding protein
7891	20686	33811	1.28	2.8E-01	AI348128.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
7891	20686	33812	1.28	2.8E-01	AI348128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U51688.1	NT	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8412	21105	34244	0.51	2.8E-01	AA911829.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8488	21180		7.34	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5'
8368	21941	35115	0.92	2.8E-01	U17251.1	NT	qf02h05.s1 NCL_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1416893 3' similar to gb:M87789 IG
9811	22264		0.88	2.8E-01	L13654.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9788	22439	35948	0.66	2.8E-01	AF132728.1	NT	602022987F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4158525 5'
							Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
							Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
							Escherichia coli translocated intimin receptor Tlr (tir) gene, complete cds

Page 76 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35947	0.86	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.52	2.8E-01	AF204903.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b;
9860	22608	35813	3.35	2.8E-01	7706163	NT	nuclear gene for mitochondrial product
10211	22859		1.47	2.8E-01	9626154	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
10251	22899	36109	0.8	2.8E-01	BE859727.2	EST_HUMAN	Fujhami sarcoma virus, complete genome
10644	23335	36573	2.42	2.8E-01	BF241062.1	EST_HUMAN	601854822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10644	23335	36874	2.42	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
10671	23362	36803	3.83	2.8E-01	BF695970.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
10794	23477	36719	1.33	2.8E-01	AF051662.1	NT	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076026 5'
11247	23609		4.51	2.8E-01	BF074023.1	EST_HUMAN	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11583	24192	37510	17.85	2.8E-01	BF074023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12408	24789		15.41	2.8E-01	D83329.1	NT	Campylobacter jejuni NCTC11168 complete genome, segment 1/6
12509	24861	31013	4.22	2.8E-01	BE178639.1	EST_HUMAN	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12632	24877	31019	1.77	2.8E-01	BE900116.1	EST_HUMAN	PM44-HT0608-030400-001-a07 HT0608 Homo sapiens cDNA
12685	25306		2.52	2.8E-01	11433629	NT	601873020F1 NIH_MGC_24 Homo sapiens cDNA clone IMAGE:3955988 5'
12806	25401		1.49	2.8E-01	AW025400.1	EST_HUMAN	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
464	13249	26890	3.97	2.7E-01	Y17324.1	NT	wu86g05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527928 3'
589	13377	26007	3.25	2.7E-01	AA450081.1	EST_HUMAN	Rattus norvegicus CDK104 mRNA
1238	13987	26654	2.13	2.7E-01	AB004908.1	NT	z039b10.s1 Soares total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1617	14384		1.58	2.7E-01	X78915.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1722	14465	27164	3.5	2.7E-01	W58087.1	EST_HUMAN	G. lamblia SR2 gene
1769	14511	27212	2.56	2.7E-01	P03341	SWISSPROT	z022h10.r1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
2131	15588		2.25	2.7E-01	AF047575.1	NT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2367	15089	27828	10.01	2.7E-01	Y13568.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2457	15175	27914	4.07	2.7E-01	A1310858.1	EST_HUMAN	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2898	15666	28314	1.2	2.7E-01	AF251276.1	NT	ta430t1.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2983	15749		2.53	2.7E-01	BF088284.1	EST_HUMAN	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
3283	16044	28693	0.88	2.7E-01	8393820	NT	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3982	16740	28374	1.97	2.7E-01	A1928015.1	EST_HUMAN	Rattus norvegicus insulin receptor (Insr), mRNA
							w092e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2492828 3'

Page 77 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4002	16749	29380	0.69	2.7E-01	AF216214.1	NT	<i>Drosophila buzzatii</i> alpha-esterase 6 (aE6) gene, partial cds
4002	16749	29381	0.69	2.7E-01	AF216214.1	NT	<i>Drosophila buzzatii</i> alpha-esterase 6 (aE6) gene, partial cds
4008	16754	29384	2.12	2.7E-01	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4980	17703		2.85	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-a03 CT0286 Homo sapiens cDNA
5011	17733	30339	2.53	2.7E-01	AA100656.1	EST_HUMAN	z190a01.r1 Stratigene colon (#937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gbX65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.53	2.7E-01	AA100656.1	EST_HUMAN	z190a01.r1 Stratigene colon (#937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gbX65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5185	17893	30308	2.39	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA4 (CHOX-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	<i>Astrocytes myrophthalma</i> mitochondrial cytochrome b, partial cds
6249	19023	31995	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31996	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6515	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6881	19598	32637	2.23	2.7E-01	Q61654	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32899	0.58	2.7E-01	U15967.1	NT	<i>Drosophila melanogaster</i> rbc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	AI540070.1	EST_HUMAN	td08h08.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7258	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7688	20266	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7588	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7638	20303	33411	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7638	20303	33412	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7694	20358	33472	0.71	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7763	20459	33583	0.68	2.7E-01	AA013147.1	EST_HUMAN	z335b11.1 Scores, retina N2b41HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

Page 78 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7825	20620		0.53	2.7E-01	AF048920.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.61	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares Infant brain T11B Homo sapiens cDNA clone IMAGE:23511 3'
8160	20884	34022	0.8	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.59	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	X03218.1	NT	Staphylococcus aureus transposon Tn564
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9700	22351	35546	0.61	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9981	22629	35838	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22866	35882	3.09	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10149	22787	36012	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22787	36013	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10724	23412	36653	3.13	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.5	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12482	25190		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24963		2.83	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12811	25054	30929	1.95	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02 5'
457	15542	25883	2.03	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	26795	1.65	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 6'
1417	14165	26848	1.14	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1889	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1889	14626	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04c10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2888451 3' similar to gb:U36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:U14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2086	14818		10.48	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2148	14878	27813	3.7	2.6E-01	M11844.1	NT	
2476	15184		1.62	2.6E-01	Y12966.1	NT	B. maritimus rbcL gene

Page 79 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	16263		8.87	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3568	16323	28971	8.99	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4079	16823	28449	0.96	2.6E-01	AW895910.1	EST_HUMAN	EST371580 IMAGE rescues, MAGF Homo sapiens cDNA
4134	16876	29506	16.7	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17246	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	aa89407.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4601	17336	29965	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PST type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4667	17401	30035	1.18	2.6E-01	AF142703.1	NT	Ophiostoma radicola maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF163350.1	NT	Mus musculus metalloprotease disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.6	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5257	18063		1.06	2.6E-01	AB035972.1	NT	Paramoecium caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	AI862398.1	EST_HUMAN	td18a03.x1 NCL_CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5688	18481	31400	0.73	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pin-2 protooncogene homolog pin-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds, and unknown g>
5880	25417		2.35	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6108	18885	31854	2.26	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6108	18885	31855	2.26	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6328	19098	32088	0.91	2.6E-01	AL192757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 6/7
6570	19334	32344	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938156 5'
6570	19334	32345	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938156 5'
6938	19673	32719	0.9	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7289	19972	33050	0.82	2.6E-01	BE148981.1	EST_HUMAN	CMO-HT0245-031199-085-f04 HT0245 Homo sapiens cDNA
7329	26110		0.78	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
7363	20044		0.89	2.6E-01	AA198149.1	EST_HUMAN	zp92e01.1 Stragagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
7639	20304	33413	1.9	2.6E-01	R10365.1	EST_HUMAN	yf37a03.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128004 3' similar to gb:U12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7687	20351	33465	0.66	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01 IN CHROMOSOME I
7748	20444	33668	1.3	2.6E-01	R02411.1	EST_HUMAN	y82a07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7804	20499	33820	1.15	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0166-181199-003-c12 HT0166 Homo sapiens cDNA
8040	20735	33867	0.84	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1.2 mannosidase (Berlin)
8040	20735	33868	0.84	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1.2 mannosidase (Berlin)
8232	20928	34064	3.05	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150396 5'
8309	21003	34140	2.13	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8594	21286	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35116	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9639	22291		0.82	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9768	22419	35628	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9768	22419	35627	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
9930	22578		0.48	2.6E-01	U67581.1	NT	Methanococcus jannaschii section 123 of 150 of the complete genome
10090	22738		0.74	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10408	23052		0.9	2.6E-01	Y10186.1	NT	Homo sapiens PHEX gene
10467	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens NRAMP2 gene for natural resistance-associated macrophage protein 2, complete cds
11400	24006	37310	1.78	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11511	24111		68.41	2.6E-01	X51755.1	NT	Human lambda-Immunoglobulin constant region complex (germline)
11996	24534		1.71	2.6E-01	10190865	NT	Mus musculus jerky (Jrk) mRNA
12177	25309		3.1	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12242	24693	31077	2.81	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced
12685	24895		1.56	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12725	24986		2.19	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039.
234	13045	25684	2.55	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA

Page 81 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
235	13045	25884	2.39	2.5E-01	4502288	NT	Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
248	13057		3.32	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
813	13584	28250	1.35	2.5E-01	U09894.1	NT	Mus musculus (C/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1038	13798		1.2	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1089	13857	26517	6.42	2.5E-01	T89937.1	EST_HUMAN	ye11g07.11 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1609	14255	28941	0.9	2.5E-01	AL115624.1	NT	Botrytis chereza strain T4 cDNA library under conditions of nitrogen deprivation
1721	14464		4.79	2.6E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1876	15581	27323	1.58	2.5E-01	BE686804.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
1878	15581	27324	1.58	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
2407	15128		16	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2500	15217		1.09	2.5E-01	AA251887.1	EST_HUMAN	zs11a12.11 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16129		0.84	2.5E-01	BF698193.1	EST_HUMAN	602125525F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4282279 5'
3407	16165		3.04	2.5E-01	AW873471.1	EST_HUMAN	EST3385464 MAGE resequences, MAGM Homo sapiens cDNA
3524	16280	28935	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3828	16579	29211	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	16579	29212	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4706	17438	30070	3.99	2.5E-01	AF007788.1	NT	Charitonera fumiferana diaphase associated protein 2 (DAP2) mRNA, complete cds
4732	17484	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE696785.1	EST_HUMAN	801437498F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922600 5'
4987	17710	30315	0.71	2.5E-01	AW873588.1	EST_HUMAN	ho6211.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041697 3' similar to WP:Y71F9A_294.D CE22858 ;
5243	18049	30878	13.48	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6870	18657	31598	0.73	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6871	18658		0.88	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6828	19285	32299	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerh-1 gene
6945	19427	32442	0.78	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA

Page 82 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7252	19936	33011	0.88	2.5E-01	U13992.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19962		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33269	0.83	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7536	20208	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33564	2.47	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7764	20460	33574	0.8	2.5E-01	BE960712.1	EST_HUMAN	801653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828198 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8268	20980	34128	0.7	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8634	21228	34368	3.87	2.5E-01	H53238.1	EST_HUMAN	yq8407.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202601 5'
8774	21468	34813	0.79	2.5E-01	M8826.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35265	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9416	22094	35265	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35263	2.06	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35264	2.06	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9898	22648	35858	1.39	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-e07 ST0186 Homo sapiens cDNA
10441	23087	36315	2.13	2.5E-01	AW152246.1	EST_HUMAN	xq40c10x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10444	23080	36319	1.21	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
11013	23685	36945	3.43	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11647	24244		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/myo-histal cotransporter (SLC5A3) gene, complete cds
11803	24393	37727	1.29	2.5E-01	U46315.1	NT	Litomosoides sigmodontis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds
11832	24490	37808	6.12	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
11980	25388		6.13	2.5E-01	AL181541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12365	24768		1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (317)
12412	25233	30821	1.37	2.5E-01	AF17072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
540	13323	25955	1.69	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
828	13688	26268	3.34	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1281	14031	28700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1281	14031	26701	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1843	14581		32.88	2.4E-01	AF287753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1893	14630	27340	1.33	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds

Page 83 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14864	27694	1.1	2.4E-01	AF111188.2	NT	Homo sapiens cerine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2165	14894		1.44	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2258	14985	27725	2.28	2.4E-01	AE000680.1	NT	Aquifex aedificus section 12 of 109 of the complete genome
2382	16104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2539	15254	27994	2.46	2.4E-01	Z36334.1	NT	O42588 28S PROTEASE REGULATORY SUBUNIT 6A;
2765	16470	28213	2.16	2.4E-01	X71783.1	NT	D discoidum (Ax2-K) ponA gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S. pombe ewi6 gene
3129	15894		2.94	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3145	15909	28554	1.48	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofitt (gag/pol) genes, complete cds
3743	16496	28131	0.73	2.4E-01	AE000312.1	NT	H. sapiens AGT gene, PstI fragment of Intron 4
4010	16756		0.74	2.4E-01	D28960.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4883	17610		1.09	2.4E-01	AL161589.2	NT	Rattus norvegicus mRNA for alpha8 crystallin-related protein, complete cds
4889	17712	30317	0.98	2.4E-01	D00944.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5375	18175	30865	0.98	2.4E-01	A1925707.1	EST_HUMAN	Hepatitis C virus genomic RNA for polyprotein, complete cds
5376	18176	30866	0.98	2.4E-01	A1925707.1	EST_HUMAN	wo33405.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	wo33405.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5569	18366	31275	8.16	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18366	31276	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5597	18592		0.77	2.4E-01	M83377.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5799	25076		0.99	2.4E-01	AJ133836.2	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
							Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
5805	18595	31520	2.22	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5895	18680	31827	3	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
5999	18780	31741	2.53	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6050	18830	31793	0.87	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6441	19209	32208	2.23	2.4E-01	AI989899.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cdAADE11 5'
7243	19928	33004	9.5	2.4E-01	L43001.1	NT	we62e11.x1 NCL CGAP_Pent1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7404	20081	33163	0.55	2.4E-01	N48732.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7625	20291	33400	0.91	2.4E-01	AF229844.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8247	20841	34078	1.61	2.4E-01	AJ012585.1	NT	yy55c11.r1 Soares_multiple sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:277460 6'
							Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
							Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8497	21189	34332	1.02	2.4E-01	BF242794.1	EST_HUMAN	60187678F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 6'
8952	21244		0.47	2.4E-01	BF678275.1	EST_HUMAN	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9030	21720	34874	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9030	21720	34875	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9463	22013	35181	7.01	2.4E-01	AI693515.1	EST_HUMAN	wd43602.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains
9603	22256	35441	0.88	2.4E-01	AF220087.1	NT	MER22 b1 TAR1 repetitive element;
9603	22256	35442	0.88	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22984	36202	1.68	2.4E-01	Q03892	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10667	23358	36598	4.6	2.4E-01	AL161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10739	23426	36671	1.39	2.4E-01	AF030199.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11158	23825		2.09	2.4E-01	Z21947.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11840	24424	37765	1.32	2.4E-01	BE617538.1	EST_HUMAN	P. asiatica mosaic virus genomic RNA
11891	24461	37801	1.75	2.4E-01	AF217491.1	NT	601441421T1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3845836 3'
12019	25180		2.34	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12287	25162		1.97	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative me7 protein (me7 gene)
12400	25201		2.06	2.4E-01	BF184542.1	EST_HUMAN	Gallus gallus gene coding for a-actin
12720	24992		3.66	2.4E-01	AL163281.2	NT	601842848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4063739 5'
380	13167	25810	1.06	2.3E-01	S75988.1	NT	Homo sapiens chromosome 21 segment HS21C081
622	13401		5	2.3E-01	U39713.1	NT	aromatase [Poephilia guttata-zebra finches, ovary, mRNA, 3188 nt]
662	13430	26069	33.31	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
913	13680	26341	4.19	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 135 of 150 of the complete genome
1558	14305		1.12	2.3E-01	U22837.2	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:35056818 5'
1599	14345	27035	1.23	2.3E-01	AJ245480.1	NT	Yersinia pestis HmsH (hmsH), HmsR (hmsR), HmsF (hmsF), and HmsS (hmsS) genes, complete cds
1628	14374	27063	2.74	2.3E-01	Y10987.2	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
2038	14772		1.51	2.3E-01	AJ295353.1	NT	Mus musculus cdh5 gene, exon 1, partial
2447	15168	27903	2.66	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2657	15367	28105	1.59	2.3E-01	MT1318.1	NT	601175662F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631015 5'
2827	14114	26789	3.38	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
2963	15729	28379	1.36	2.3E-01	AA601379.1	EST_HUMAN	Marinibacteria agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain JFO 14957
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	no16d08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
							repetitive element/contains element THR repetitive element;
							yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

Page 85 of 536  
Table 4

## Single Exon Probes Expressed in Brain

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3363	16122	28780	1.14	2.3E-01	H69838.1	EST_HUMAN	y97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3821	16573	29205	1.01	2.3E-01	S82821.1	NT	GSTA9-glutathione S-transferase Yc2 subunit (5' region, Intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3914	16684		6.22	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4316	17055	29880	1.1	2.3E-01	R82252.1	EST_HUMAN	y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4368	17106		1.98	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4417	17153	29784	1.03	2.3E-01	D90899.1	NT	Synechocystis sp. PCC8803 complete genome, 1/27, 1-133859
4454	17190	29816	2.51	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4517	17252	29887	6.19	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4988	17711	30316	0.84	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5221	18028	30854	2.53	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.06	2.3E-01	BF059381.1	EST_HUMAN	7k30b05.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476899 3' similar to SW:GAG_SMSAV P03330 GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
5443	18242	31130	4.58	2.3E-01	X66587.1	NT	C.familialis rom1 gene
5563	18360		0.94	2.3E-01	L30112.1	NT	Vitisformis cornum small subunit ribosomal RNA gene
5685	18460	31374	0.76	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
5851	18638	31575	1.59	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5851	18638	31576	1.59	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6558	19323	32330	0.93	2.3E-01	AF198089.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit Via (coxVia2) mRNA, complete cds; nuclear gene for mitochondrial product
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element
7011	19703	32759	1.08	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7186	19874	32947	0.9	2.3E-01	AF000227.1	NT	Sesale cereale omega secalin gene, complete cds
7315	19998	33077	3.14	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7318	20001	33078	0.84	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7318	20001	33080	0.84	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7508	20179		2.84	2.3E-01	6754778	NT	Mus musculus myosin XV (Myo15), mRNA
7513	20184	33278	1.38	2.3E-01	BE886071.1	EST_HUMAN	601511573F1 NIH_MGC-71 Homo sapiens cDNA clone IMAGE:3912859 5'
7652	20316		2.73	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
7760	20446	33569	0.71	2.3E-01	AL161598.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 58

Page 86 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20587	33717	2.18	2.3E-01	M88931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha elanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57089.1	NT	Mus musculus prosaposin (psapISGP-1) gene, complete cds
8971	21363	34510	0.56	2.3E-01	AW090541.1	EST_HUMAN	xs90s08.x1 NCJ CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591534 3'
8788	21478	34827	0.45	2.3E-01	AW084460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9039	21729	34984	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9480	22133	35313	0.82	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Plk3cd), mRNA
9609	22262	35448	0.62	2.3E-01	U77974.1	NT	Tribolium castaneum transcription factor homolog (Tc-ewe) gene, complete cds
9828	22281	35471	0.5	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2866739 5'
9882	22334	35529	0.59	2.3E-01	AW064460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
8767	22418	35825	0.59	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-f04 DT0036 Homo sapiens cDNA
9834	22485	35888	2.45	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0558-240400-014-g11 HT0558 Homo sapiens cDNA
9882	22542	35734	2.75	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10340	22987	36205	0.84	2.3E-01	AF201928.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22998		5.11	2.3E-01	BF133577.1	EST_HUMAN	601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10937	23617	36867	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23817	36868	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ260189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ260189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
11815	24403		1.75	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11855	24439		1.33	2.3E-01	6006010	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12088	24693		4.88	2.3E-01	T27281.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
12120	24812		1.62	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
12173	25319	30711	2.88	2.3E-01	AW303623.1	EST_HUMAN	xs21d07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
12206	25366	30813	8.63	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2 :contains PTR5.b2 TAR1 repetitive element ;
12255	24701		2.51	2.3E-01	BF683319.1	EST_HUMAN	601807202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
						EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'

Page 87 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12303	24728		2.35	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12398	24784		1.76	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlk-3 (PwDlk-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12847	24952		2	2.3E-01	BF475611.1	EST_HUMAN	ncs38h12.x1 Lupskl_sclatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
88	12814	25562	1.63	2.2E-01	AI062190.1	EST_HUMAN	MER38 repetitive element ;
1557	14304	28993	1.84	2.2E-01	AF187850.1	NT	ox14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875290 3' similar to
2082	14814	27547	2.52	2.2E-01	MS4840.1	NT	TRQ13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2402	15123	27860	6.3	2.2E-01	BF877638.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2594	15308	28044	2.02	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2594	15308	28045	2.02	2.2E-01	BE618258.1	EST_HUMAN	602086608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
2884	15651	28294	4.36	2.2E-01	BE156625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2884	15651	28295	4.36	2.2E-01	BE156625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2821	15687		1.57	2.2E-01	AF020503.1	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
3387	16148		1.97	2.2E-01	AL181562.2	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
3794	16548		1.12	2.2E-01	AF155728.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4105	16848		0.72	2.2E-01	U68174.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4194	16935	29562	6.45	2.2E-01	AF155142.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4232	16973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4232	16973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4323	17062	29889	1.21	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4323	17062	29890	1.21	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4775	17507		1.36	2.2E-01	D50804.1	NT	Human scRNA (BC200 beta) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP6) pseudogene
4982	17705		1.1	2.2E-01	L13289.1	NT	zq87c05.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:648988 5'
5082	17781		0.93	2.2E-01	S57565.1	NT	Mus musculus vinculin gene, exon 3
5140	17858	30474	2.84	2.2E-01	5835974	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5559	18454	31368	2.07	2.2E-01	5803002	NT	Vidia chalybeata mitochondrion, complete genome
5669	18464		4.5	2.2E-01	D64000.1	NT	Homo sapiens diaphanous (Drosophila, homolog 2 (DIAPH2), transcript variant 156, mRNA
5910	18694	31646	0.56	2.2E-01	U67087.1	NT	Synechocystis sp. PCC8603 complete genome, 19/27, 2392728-2538999
5910	18694	31647	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
							Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds

Page 88 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6608	19369	32381	0.73	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
6928	19682	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7029	19721	32777	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spbA) genes, complete cds; and unknown genes
7029	19721	32778	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spbA) genes, complete cds; and unknown genes
7191	19877	32950	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7191	19877	32951	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7386	20066	33144	0.63	2.2E-01	AE000352.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7628	20294	33402	0.66	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain: C-125
7919	20614		2.04	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7987	20682	33808	1.01	2.2E-01	Z49933.1	NT	E. coli sepA and sepB genes
8449	21141	34279	0.54	2.2E-01	AJ132818.1	NT	Pan troglodytes MeCP2 gene 3'UTR
8794	21486	34632	3.53	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8920	21611		4.35	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
9013	21703	34853	1.46	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9098	21786	34952	1.04	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9189	21859	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	za04f08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:281591 5'
9207	22086	35259	13.43	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9252	21931	35104	0.69	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xkps)
9263	22017	35185	0.81	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9276	22030	35200	3.95	2.2E-01	M89943.1	NT	Brachydanio rerio opendymin beta and gamma chains (Epo) gene, complete cds
9521	22174	35358	0.58	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
9715	22368	35584	3.4	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPaHSP21) mRNA, complete cds; nuclear gene for chloroplast product
9853	22503	35703	1.95	2.2E-01	BF206307.1	EST_HUMAN	601869724F.1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10076	22724	35841	0.95	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10232	22880	36092	0.6	2.2E-01	T59472.1	EST_HUMAN	y63d08.r1 Stratagene ovary (H937217) Homo sapiens cDNA clone IMAGE:75855 5'
10232	22880	36093	0.5	2.2E-01	T59472.1	EST_HUMAN	y63d08.r1 Stratagene ovary (H937217) Homo sapiens cDNA clone IMAGE:75855 5'
10268	22916	36126	0.58	2.2E-01	AF068264.1	NT	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyridoxaldehyde quinone synthesis A (pqxA) genes, complete cds; and pyridoxin>
10341	22988		0.81	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds

Page 89 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10387	23033	36247	0.8	2.2E-01	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.8	2.2E-01	AE001592.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23168	36384	0.48	2.2E-01	AF048720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.58	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.46	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11389	24005	37309	4.83	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11438	23205	36437	5.22	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC61580), mRNA
11835	24493		1.86	2.2E-01	BE870959.1	EST_HUMAN	601446957 F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850870 5'
12040	25380		2.21	2.2E-01	U82871.2	NT	Homo sapiens melanoma antigen Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12123	24615		2.19	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12225	17804	30581	3.87	2.2E-01	AW361088.1	EST_HUMAN	RC1-C10249-141198-021-g04 C10249 Homo sapiens cDNA
12226	24691		1.6	2.2E-01	AW661922.1	EST_HUMAN	h117602.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872523 3'
12731	25371		2.58	2.2E-01	AV694801.1	EST_HUMAN	AV684801 GKC Homo sapiens cDNA clone GKCAH802 5'
950	13716	26382	2.12	2.1E-01	AA668289.1	EST_HUMAN	nm31e11.s1 NCL CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26394	0.77	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1102	13859		2.76	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1176	13929	26593	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1176	13929	26594	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1908	14843	27353	2.07	2.1E-01	AA906824.1	EST_HUMAN	ok73802 st NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518810 3' similar to gb:K02765
2152	14882	27816	4.2	2.1E-01	BF696073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2485	15396	27842	1	2.1E-01	H73988.1	EST_HUMAN	602083129 F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2485	15396	27843	1	2.1E-01	H73988.1	EST_HUMAN	yu04f07.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837 3'
2568	15270	28005	0.91	2.1E-01	AF022814.1	NT	yu04f07.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837 3'
2925	15891	28335	2.3	2.1E-01	6812445	NT	Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
3786	16538		6.08	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4032	16777	28408	1.1	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082		1.77	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4537	17272	28904	1.23	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5013	17734	30341	1.4	2.1E-01	Q01338	SWISSPROT	Homo sapiens pshap47 gene, complete cds
							ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

Page 90 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	17809	30426	1.09	2.1E-01	AE001626.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218	18028	30650	6.24	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6787	19531	32559	1.4	2.1E-01	AJ23392.1	NT	Dato fragilis mitochondrial 16S rRNA gene, partial
6798	19469	32481	1.92	2.1E-01	U04942.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7306	19889	33065	0.85	2.1E-01	Q01958	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7308	19889	33066	0.85	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000		2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7608	20272	33380	1.84	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7651	20315	33425	1.22	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7651	20315	33426	1.22	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7671	20668		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8400	21083	34229	4.44	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds
8696	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
8698	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
8857	21548		0.45	2.1E-01	AB022524.1	NT	Homo sapiens APOL gene, exon 9
8935	21626	34768	5.68	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025W
9404	22068	35237	0.57	2.1E-01	N42535.1	EST_HUMAN	yy1te10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270954 5'
9404	22066	35238	0.57	2.1E-01	N42538.1	EST_HUMAN	yy1te10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270954 5'
9413	22091	35262	2.31	2.1E-01	X97378.1	NT	A. thaliana mRNA for AtRanBP1b protein
9518	22171	35354	1.13	2.1E-01	AB036528.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22876	36088	1.47	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10258	22808	36116	2.5	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10264	22912	36122	0.97	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11554	24153		2.19	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b1 HT0622 Homo sapiens cDNA
11870	24944		1.38	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12377	24775		2.07	2.1E-01	AF217480.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12578	25287		1.47	2.1E-01	L32588.1	NT	Human granulosa gene
12635	24935		1.42	2.1E-01	BE622149.1	EST_HUMAN	801440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'

Page 91 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12768	25019	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a59a02.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:3223034 3'
185	13008	25950	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC61008), mRNA
683	13458	26103	1.24	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
782	13564	26225	2.19	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
981	13753	26414	1.09	2.0E-01	D90805.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915
1103	13960	26519	2.47	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1232	13981	26551	1.77	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1285	14035	26708	1.63	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c08 HT0422 Homo sapiens cDNA
1443	14180		1.52	2.0E-01	AJ243997.1	NT	Plum pox virus strain M, complete genome, isolate PS
1470	14217	26804	14.63	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1544	14290	26977	1.97	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0605
1550	14298	26983	1.01	2.0E-01	AF260700.1	NT	Homo sapiens sodium iodide symporter mRNA, partial cds
1692	14438	27132	1.4	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1712	14455		1.67	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1752	14494		4.33	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1883	14820	27329	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:38533330 5'
1883	14820	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:38533330 6'
2347	15070		1.63	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3693	16447	29087	0.89	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3822	16574	29208	1.12	2.0E-01	AL163204.2	NT	GED-11 PROTEIN
3938	16888	29327	0.76	2.0E-01	Z46906.1	NT	Homo sapiens chromosome 21 segment HS21C004
4528	17263		8.49	2.0E-01	BE826165.1	EST_HUMAN	Sus scrofa
4979	17702	30309	5.26	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5009	18237	28893	0.8	2.0E-01	P46607	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5359	18161	30845	2.63	2.0E-01	X56600.1	NT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5655	18450	31363	1.94	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5750	18542	31464	0.76	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5969	18751	31712	6.3	2.0E-01	U15900.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6081	18860		0.73	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6102	18968	31943	0.79	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6335	19105	32094	3.2	2.0E-01	X61033.1	NT	Mauritius mu class glutathione transferase gene
6435	19203	32200	4.02	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141089-001-g06 CT0247 Homo sapiens cDNA
7194	19880	32954	1.26	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (PfkC) gene, exons 3 through 7
7345	20026	33102	0.69	2.0E-01	P64422	SWISSPROT	GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR
7676	20339	33452	0.84	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7653	20548		5.9	2.0E-01	AF028028.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33925	2.95	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8824	21316		0.99	2.0E-01	BE562247.1	EST_HUMAN	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9251	21930	35103	0.82	2.0E-01	U82511.1	NT	Dictyostellium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9290	21957	35129	0.69	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9456	22006		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9646	22298	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22689	35792	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22689	35793	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10067	22715	35933	0.88	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10067	22715	35934	0.88	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22762		0.69	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10305	22952	36167	2.78	2.0E-01	X87121.1	NT	R.norvegicus mRNA for NTR2 receptor
10744	23431	36874	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
10744	23431	36875	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11609	24207	37530	1.4	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37531	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.51	2.0E-01	AF2068637.2	NT	Pinophytes promiella liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12545	25210		1.39	2.0E-01	AF020773.1	NT	Homo sapiens rhinein-Lm isoform (rhinein) mRNA, complete cds
12556	25139	30894	1.36	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12564	24950	30985	3.58	2.0E-01	A023592.1	EST_HUMAN	ov80a10.s1 Scars testis_NHT Homo sapiens cDNA clone IMAGE:1043610 3'
12618	24924		2.68	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30978	1.87	2.0E-01	11528495	NT	Mus musculus fructose 3 kinase (Fr3k), mRNA
108	12929		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlt1), mRNA
342	13143	25781	6.86	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	26058	1.43	1.9E-01	U32551.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
641	13420	26059	1.43	1.9E-01	U32551.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds

Page 93 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	26066	6.97	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
649	13427	26066	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
965	13730		1.73	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1082	13840	26499	13.43	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 6' end
1349	14097	26772	1.76	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2380	15102	27841	3.61	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10681), mRNA
2923	15689	28333	3.43	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2939	15704		6.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3002	16768	28417	0.96	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3390	16149	28803	4.26	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	R16467.1	EST_HUMAN	yf42f10.t Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3818	16668	29189	1.33	1.9E-01	P99768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3973	16722	29366	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4063	16808	29438	1.28	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4208	16947	29573	1.09	1.9E-01	BE634943.1	EST_HUMAN	MR1-FN0010-290700-007-404 FN0010 Homo sapiens cDNA
4950	17677		1.05	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2618444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5558	18355	31285	7.87	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5749	18541	31463	0.7	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5795	18566		2.58	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6235	19009	31965	0.75	1.9E-01	A1762391.1	EST_HUMAN	w154h02.x1 NCI_CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2394099 3'
6294	19067	32050	1.03	1.9E-01	AW148452.1	EST_HUMAN	x14c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
6376	17952	30548	1.69	1.9E-01	R43212.1	EST_HUMAN	y909a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
6900	18638	32682	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
6900	18638	32683	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7160	18847	32917	0.62	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7391	20070	33149	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7436	20113	33201	3.11	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sber1) gene, complete cds
7865	20560	33709	1.46	1.9E-01	AL161567.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8586	21278	34417	10.77	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds

Page 94 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21536	34681	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8844	21536	34682	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9776	22428	35632	0.61	1.9E-01	AA912486.1	EST_HUMAN	086g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537508 3' similar to contains Alu repetitive element;
10142	22780	36005	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
10142	22780	36006	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10640	23237	36470	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10640	23237	36471	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	36583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10988	23661	36915	1.34	1.9E-01	AA912480.1	EST_HUMAN	086f02.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gbL21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
10988	23661	36916	1.34	1.9E-01	AA912480.1	EST_HUMAN	086f02.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gbL21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
11487	24088	37399	1.53	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
11726	24320	37645	2.77	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37673	1.6	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12399	24785	38683	1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
30	12858	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022060.1	NT	Mus musculus Ccig gene for chaperonin containing TGP-1 gamma subunit, partial cds
361	13159	25802	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	26158	1.01	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13728	26390	0.94	1.8E-01	AJ012212.1	EST_HUMAN	wd71f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1089	13828	26485	1.63	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1266	14015	26683	6.26	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26925	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26926	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1839	14577		1.2	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14697		1.68	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;

Page 95 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14845	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2697	15406		2.36	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT00718-081289-036-g04 DT00718 Homo sapiens cDNA
2898	15865		1.89	1.8E-01	AF184599.1	NT	Jonopsidium scale LEAFY protein (LEAFY2) gene, partial cds
2904	15670	28319	1.29	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659759 3'
3121	15866	28626	1.76	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3610	16363	29005	0.88	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element
3610	16363	29006	0.88	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element
4299	17038		1.43	1.8E-01	D37894.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4519	17254	29888	5.94	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4721	17453	30087	2.9	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17486	30114	0.94	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4984	17707	30311	2.03	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g08 ST0203 Homo sapiens cDNA
4996	17722	30325	1.06	1.8E-01	AI792382.1	EST_HUMAN	an28g07.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5036	17754	30387	4.66	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5835	18624	31558	0.68	1.8E-01	N28629.1	EST_HUMAN	yx38h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264063 5'
6037	18817	31777	1.18	1.8E-01		NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6037	18817	31778	1.18	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6419	19187	32185	1.15	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6463	19230		2.08	1.8E-01	N94853.1	EST_HUMAN	y62h02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6906	19844	32699	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wssu, complete cds
6908	19844	32690	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wssu, complete cds
7346	20027	33103	0.7	1.8E-01	AP001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
9242	21921	35091	1.23	1.8E-01	U73256.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9274	22028	35198	1.22	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9391	22053		0.5	1.8E-01	AA493751.1	EST_HUMAN	nh02a05.e1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element;
9473	22126	35305	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE

Page 96 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22128	35308	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	0.91	1.8E-01	M26019.1	NT	S. commune orotidine-5'-phosphate decarboxylase (URAT1) gene, complete cds
9514	22167	35348	0.91	1.8E-01	M26019.1	NT	S. commune orotidine-5'-phosphate decarboxylase (URAT1) gene, complete cds
9679	22331	35326	0.75	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9683	22335	35330	0.77	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10033	22681		0.78	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10288	22914	36124	1.48	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	36465	3.08	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U39508.1	NT	Bacteriophage r11 integrase, repressor protein (iro), dUTPase, holin and lysin genes, complete cds
10637	19644	32889	2.61	1.8E-01	AB018561.1	NT	Citrus latifolius mRNA for vsus, complete cds
10637	19644	32890	2.61	1.8E-01	AB018561.1	NT	Citrus latifolius mRNA for vsus, complete cds
10638	23329	36567	5.69	1.8E-01	AF019107.1	NT	Dictyostellium discoideum unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X57033.1	NT	B. taurus mRNA for potassium channel
11767	24358	37691	3.45	1.8E-01	8594421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11987	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12478	24839		3.28	1.8E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12583	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hxx1)
12746	26324		1.61	1.8E-01	X16635.1	NT	Rattus norvegicus CaBP9k gene
563	13345	25972	1.57	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
787	13659	26221	2.32	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1036	13796	28455	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1036	13796	28456	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1874	14710		2.6	1.7E-01	AF255051.1	NT	Homo sapiens BNI(3H) (BNI(3H)) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28275	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (haptR) gene, complete cds, and YRAL VIBCO gene, partial cds

Page 97 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2863	15631	28276	2.28	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15693	28338	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3103	15968	28508	1.24	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3665	16348	28989	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3816	16369		0.92	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16668	29309	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial Intron 10 of the ALL-1/MLL/HRX gene fused to Intron 5 of the AF-4/JEL gene
4522	17257		1.69	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	AJ247635.1	EST_HUMAN	qh57609.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 OFR repetitive element;
5054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5122	17840	30456	0.75	1.7E-01	D37851.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18126	30785	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5323	18126	30786	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5506	18304	31205	0.62	1.7E-01	U43569.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6237	19011	31986	13.23	1.7E-01	H72118.1	EST_HUMAN	ys02q06.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19066	32048	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6293	19066	32049	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6753	17922	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	600844067T1 NIH_JMGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6780	19324		2.28	1.7E-01	AF026562.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
6902	19340		0.88	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7120	19808	32874	1.1	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sekai-V72 prophage inserted region
7197	19883	32957	8.8	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_JMGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7380	20060	33139	1.37	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
7396	25112	33153	0.71	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7760	20456	33580	1.32	1.7E-01	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds

Page 98 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7863	20568	35684	0.62	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8175	20869	34001	6.19	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8176	20869	34002	6.19	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8598	21290	34431	0.47	1.7E-01	AW892873.1	EST_HUMAN	RC2-BN0032-120200-011-at10 BN0032 Homo sapiens cDNA
8628	21320	34462	2.09	1.7E-01	D00394.1	NT	Rat (SHR strain) SX1 gene
8743	21435	34580	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9068	21755	34918	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9068	21755	34917	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9490	22143	35323	7.85	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22280	35435	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST1389584 MAGe resequences, MAGO Homo sapiens cDNA
9597	22250	35436	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST1389584 MAGe resequences, MAGO Homo sapiens cDNA
9615	22268	35455	3.14	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22359	35555	0.63	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-8), (sp8 gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10293	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10295	22942	36156	1.72	1.7E-01	AA627972.1	EST_HUMAN	nc80e07.at NCJ_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gb:L28081
10501	23147		0.45	1.7E-01	AL181542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN); Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10579	23274	36511	8.78	1.7E-01	BE380835.1	EST_HUMAN	601288547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10709	23398	36637	2.65	1.7E-01	AA814617.1	EST_HUMAN	of43a03.s1 NCJ_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11055	23725	36989	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11055	23725	36998	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11146	23813	37096	1.62	1.7E-01	Y08391.1	NT	S.pombe pop1+ gene
11348	24038	37341	1.69	1.7E-01	AA883375.1	EST_HUMAN	al45f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
11712	24307		1.83	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
11746	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
11746	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
11874	24453	37799	2.62	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12000	25320		1.95	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 99 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12288	25197		1.65	1.7E-01	A1824404.1	EST_HUMAN	tx69g05.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC
12552	24889	30998	16.27	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
122	12940	25592	2.38	1.6E-01	AF217532.1	NT	Human beta globin region on chromosome 11
894	15518	28081	1.51	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1493	14240	26927	1.16	1.6E-01	AA548563.1	EST_HUMAN	yt75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1612	14268	26944	3.82	1.6E-01	AF298117.1	NT	nk28d12.st NCL CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014839 3'
1917	14654	27394	1.86	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1977	14713		1.51	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2383	16693	27844	1.36	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2497	15214	27957	1.4	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2894	15661	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	16661	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3982	16730		2.49	1.6E-01	AE004413.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4294	17033	29681	9.42	1.6E-01	AF179680.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4423	17159		3.07	1.6E-01	AW986801.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
4431	17167		4.35	1.6E-01	6763319	NT	EST380677 IMAGE rescues, MAGJ Homo sapiens cDNA
							Mus musculus chaperonin subunit 3 (gamma) (Cci3), mRNA
4869	17696	30219	0.7	1.6E-01	P40631	SWISSPROT	MIORNUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
							PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4892	17619	30237	1.38	1.6E-01	AA088943.1	EST_HUMAN	z84h09.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:511381 3' similar to TR:E221955
4911	17639	30253	1.54	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4911	17639	30254	1.54	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5303	18108	30768	0.89	1.6E-01	L40608.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
							Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5435	18234	30947	2.95	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
							HYPOHETICAL 127.6 KD PROTEIN ;
5495	18234	30948	2.95	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5447	18246	31134	2.15	1.6E-01	AF034716.1	NT	HYPOHETICAL 127.6 KD PROTEIN ;
5938	18720	31679	0.83	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebp) gene, complete cds
6192	18939	31909	0.71	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6162	18939	31910	0.71	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'

Page 100 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6334	19104	32092	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6334	19104	32093	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6885	19602	32641	0.55	1.6E-01	A4398047.1	EST_HUMAN	z88004.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
6887	17944	30539	5.32	1.6E-01	AW291215.1	EST_HUMAN	UI-H-B12-agi-b-06-Q-UI.s1 NC1 CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7678	20340	33453	1.66	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8018	20713	33844	0.87	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8530	21222	34364	0.88	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
8725	21417	34561	0.63	1.6E-01	R13673.1	EST_HUMAN	y60h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
8831	21523		0.59	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21661	34708	1.72	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9009	21699		0.83	1.6E-01	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041189-011-h01 ST0200 Homo sapiens cDNA
9554	22207	35391	1.7	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9589	22242		0.87	1.6E-01	BE155684.1	EST_HUMAN	PM2-HT0363-270100-004-f11 HT0353 Homo sapiens cDNA
10553	23249	36488	3.3	1.6E-01	AW850553.1	EST_HUMAN	IL3-C10220-11189-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36846	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11089	23729		4.28	1.6E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23984	37296	7.28	1.6E-01	6871652	NT	Mus musculus adaptor-related protein complex AP-4, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.26	1.6E-01	BF527237.1	EST_HUMAN	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11866	25331		1.64	1.6E-01	6879466	NT	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12002	24538	37273	5.28	1.6E-01	AV719585.1	EST_HUMAN	Rat convertase PC5 mRNA, 5' end
12292	24721	31052	1.72	1.6E-01	L14933.1	NT	RC1-L1T0074-120200-014-h01_1 L1T0074 Homo sapiens cDNA
12321	24740		1.5	1.6E-01	AW839711.1	EST_HUMAN	Cucumis sativus KS mRNA for anti-kaurine synthase, complete cds
12418	25149		287.76	1.6E-01	AB045310.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12574	24901		2.4	1.6E-01	AK024496.1	NT	

Page 101 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12661	24931		1.72	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds, nuclear gene for mitochondrial product
12687	24973	30692	1.7	1.6E-01	8506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12706	25046		1.62	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
241	13050	25689	1.4	1.9E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
241	13050	25690	1.4	1.9E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
673	16517		9.31	1.9E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	13539	26168	1.09	1.9E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.9E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1076	13833	26491	2.75	1.9E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1091	13849		1.42	1.9E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13946	26610	0.82	1.9E-01	AW195516.1	EST_HUMAN	x139d1.1 x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1252	14001	26668	2.96	1.9E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1252	14001	26669	2.96	1.9E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1465	14212	26901	1.86	1.9E-01	AF117340.1	NT	Mus musculus MAP Kinase Kinase 1 (Mekk1) mRNA, complete cds
1901	14638	27347	1	1.9E-01	AW444451.1	EST_HUMAN	UI-H-B13-akb-b-09-0-JL.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2716	15423	28162	1.98	1.9E-01	BF695381.1	EST_HUMAN	602063269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2914	15680		1.15	1.6E-01	AW672516.1	EST_HUMAN	xw56a02.x2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1
3048	15814	28459	0.74	1.9E-01	O76687	SWISSPROT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3347	16106	28761	5.06	1.9E-01	AA835049.1	EST_HUMAN	0088005.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1671337 3' similar to gb:M11433
3361	16120	28777	0.82	1.9E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3361	16120	28778	0.82	1.9E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3798	16491	29126	2.11	1.9E-01	U09934.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3752	16504	29140	0.74	1.9E-01	7108358	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3848	16699	29236	2.65	1.9E-01	AW665983.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4028	16773	29405	1.1	1.9E-01	AW366659.1	EST_HUMAN	h10106.x1 Scarses_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4161	16901	29530	8.35	1.9E-01	AL163284.2	NT	RC2-HT0149-191089-012-c08 HT0149 Homo sapiens cDNA
4876	17410	30046	1.67	1.9E-01	BF687665.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4703	15423	28162	1.82	1.9E-01	BF693381.1	EST_HUMAN	602067192F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4069223 5'
5132	17650	30487	1.55	1.9E-01	Z72608.1	NT	602063269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
							S.cerevisiae chromosome VII reading frame ORF YGL086w

Page 102 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5145	17664	30480	1.05	1.5E-01	AF563113.1	NT	Mouse exallitis gonadotropin-releasing hormone type II gene, complete cds
5175	17684	30499	2.16	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	AF256652.1	NT	Calman crocodilus MHC class II beta chain (hclibeta) gene, complete cds
5243	18031		6.92	1.5E-01	P15186	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5451	18250	31139	5.08	1.5E-01	AW650754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5492	18291	31198	8.42	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5492	18291	31199	8.42	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5915	18700	31653	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5916	18700	31654	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5952	18734	31693	1.93	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6102	18860	31847	3.1	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6162	18928		1.77	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6281	19025	31999	2.09	1.5E-01	AF143407.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6409	25089	32176	2.21	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6437	18205	32201	4.99	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
6448	18216	32214	1.85	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6493	18259	32260	2.35	1.5E-01	Q28492	SWISSPROT	AMELOGENIN
6585	18348	32381	1.25	1.5E-01	AA714760.1	EST_HUMAN	rw30d10.s1 NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241871 3'
6612	19375	32389	1.66	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6882	17958	30554	6.82	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	ob73f02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element
7115	19803		2.07	1.5E-01	AF210842.1	NT	LTR2 repetitive element
7280	18973	33051	2.86	1.5E-01	AJ973157.1	EST_HUMAN	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7480	20162	33254	2.04	1.5E-01	AF299073.1	NT	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7480	20162	33256	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7489	20171	33282	2.04	1.5E-01	AW500811.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7489	20171	33283	2.04	1.5E-01	AW500811.1	EST_HUMAN	UIHF-BNO-akk-d-05-0-UI.F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	U46560.1	NT	UIHF-BNO-akk-d-05-0-UI.F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7857	20652	33775	0.86	1.5E-01	P21303	SWISSPROT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
							MEROZOTIN RECEPTOR PK66 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Page 103 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.s1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8211	20905		0.95	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8299	20993		11.54	1.5E-01	C16800.1	EST_HUMAN	6071510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8332	21025	34162	1.8	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-528H09 5'
8491	21183	34325	1.65	1.5E-01	D84476.1	NT	Pangasinanodon gligas growth hormone (GH) mRNA, complete cds
8512	21204		0.71	1.5E-01	P43448	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8737	21429	34575	1.16	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9002	21692	34842	2.88	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9092	21781	34945	1	1.5E-01	BF685465.1	EST_HUMAN	zaf59e06.s1 Soares fetal liver spleen cDNA clone IMAGE:298866 3' similar to PIR:S44443 S44443 RAD23 protein homolog 2 - human;
9100	21788		2.3	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9305	21972		0.74	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9717	22368	35566	0.53	1.5E-01	M77144.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
9821	22472	35674	7.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9821	22472	35675	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10103	22751	35965	2.92	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10207	22855	36070	2.18	1.5E-01	A1814046.1	EST_HUMAN	P. lentusculus mRNA for Integrin beta subunit
10207	22855	36071	2.16	1.5E-01	A1814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10285	22933	36148	2.01	1.5E-01	U40932.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36311	1.43	1.5E-01	AJ011984.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36312	1.43	1.5E-01	AJ011984.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10595	23289	36527	1.62	1.5E-01	BE088492.1	EST_HUMAN	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10595	23289	36528	1.62	1.5E-01	BE088492.1	EST_HUMAN	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10726	23414	36654	7.31	1.5E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
10726	23414	36655	7.31	1.5E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
10898	23576		1.7	1.5E-01	AB042975.1	NT	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11012	23684	36944	1.8	1.5E-01	AW841915.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11057	23727	36999	1.85	1.5E-01	AA425488.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA

Page 104 of 536  
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Single Exon Probes Expressed in Brain

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11119	19873	33051	1.69	1.5E-01	A1973167.1	EST_HUMAN	wf62c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11625	24222		1.56	1.5E-01	A1193704.1	EST_HUMAN	qe72e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
11959	26202		11.07	1.5E-01	BF700592.1	EST_HUMAN	602128753F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286549 5'
12320	24739		1.37	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12324	24743		1.77	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterat-1 (Dio-1)
12369	24771		5.35	1.5E-01	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12385	25220		9.97	1.5E-01	R83077.1	EST_HUMAN	ye87e04.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	AV741272.1	EST_HUMAN	AV741272 OB Homo sapiens cDNA clone CBDA004 5'
12573	25150	30897	9.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12783	26036	30865	1.89	1.5E-01	AJ278242.1	NT	Sus scrofa mRNA for sodium iodide symporter
292	13098		1.72	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV856P to TCRBV21S2A2 region
890	13659		3.62	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5'-methyltransferase, complete cds)
1236	13985		2.48	1.4E-01	T91884.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:112032 3'
1742	14484		1.5	1.4E-01	6678980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27186	1.71	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
1898	14635		0.96	1.4E-01	AW135741.1	EST_HUMAN	U1-H-B11-act-e-09-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1978	14714		9.33	1.4E-01	AA720615.1	EST_HUMAN	hy72d07.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1283821 3'
2478	15198	27936	1.39	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2795	15500	28241	4.23	1.4E-01	A1933456.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441668 3'
3879	16629	29267	0.96	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
3879	16629	29268	0.96	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
4153	18895	29524	8.99	1.4E-01	A1699094.1	EST_HUMAN	bs6c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4153	18895	29525	8.89	1.4E-01	A1699094.1	EST_HUMAN	bs6c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16963	29577	3.73	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
5014	17735	30342	0.94	1.4E-01	U12883.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30658	5.48	1.4E-01	T90877.1	EST_HUMAN	ye15c11.s1 Striatagene lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
5246	18052	30879	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5246	18052	30880	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6205	19890	31959	3	1.4E-01	BE326891.1	EST_HUMAN	ht67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:313538 3'
6391	19160	32160	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19160	32161	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2681761 3'

Page 105 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6600	19267		1.64	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6509	19274	32275	2.45	1.4E-01	BF378533.1	EST_HUMAN	QV1-JUN0036-080300-103-409 UM0036 Homo sapiens cDNA
7026	19718		0.85	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7284	19967		1.51	1.4E-01	AW015373.1	EST_HUMAN	U1-H-BIO-aat-c-09-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7521	20192	33283	1.19	1.4E-01	U85845.1	NT	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
7653	20317	33427	0.98	1.4E-01	AI305192.1	EST_HUMAN	q190b12.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8373	21068		1.23	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH08 3'
8683	21375		0.57	1.4E-01	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 O02710 GAG POLYPROTEIN.
8811	21503	34650	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21583	34722	0.59	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9021	21711	34864	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9085	21774	34938	8.81	1.4E-01	BF310959.1	EST_HUMAN	6011885465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	W93411.1	EST_HUMAN	z094a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9246	21825	35095	0.46	1.4E-01	X73293.1	NT	M. vanrelli genes rpoH, rpoB and rpoA
9248	21826	35098	0.46	1.4E-01	X73293.1	NT	M. vanrelli genes rpoH, rpoB and rpoA
9258	21837	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9258	21837	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.96	1.4E-01	AF121391.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a (JAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35551	0.97	1.4E-01	X66092.1	NT	C. parvifrons ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023813.1	NT	Macromitrium levalum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9888	22636	35846	0.56	1.4E-01	AW021608.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9888	22636	35847	0.56	1.4E-01	AW021608.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22805	36022	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84293.1	EST_HUMAN	y447d03.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:111365 5'
10489	23145	36372	0.82	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2812870
10607	23301		1.84	1.4E-01	AA811480.1	EST_HUMAN	oa99e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
10746	23433	36878	3.24	1.4E-01	R63400.1	EST_HUMAN	y170c05.r1 Soares breast 2Nb1Bst Homo sapiens cDNA clone IMAGE:154088 5'
10954	23631	36879	1.31	1.4E-01	AW104982.1	EST_HUMAN	xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'

Page 106 of 536  
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11036	23707	36976	1.3	1.4E-01	T06102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120930 5'
11036	23707	36976	1.3	1.4E-01	T06102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23709	36979	2.35	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11262	23924	37215	1.68	1.4E-01	X68092.1	NT	C.perfringens ORF for putative membrane transport protein
11301	19967		1.41	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-eat-c-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11512	24112		1.82	1.4E-01	X62102.1	NT	M.musculus p16K gene for 16 kDa protein
11743	24335	37681	1.83	1.4E-01	AF146789.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and HBAR (Hbar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW684572.1	EST_HUMAN	h114h08.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972319 3'
11827	24411	37748	1.31	1.4E-01	AW684572.1	EST_HUMAN	h114h08.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972319 3'
12213	25172	30904	1.98	1.4E-01	AB000890.1	NT	Ephydratia fluidalis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12276	24714		2.2	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
12318	25393		2.84	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12413	24784		1.35	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27. 2889767-3002865
12500	25407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		6.26	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
12779	25033		2.37	1.4E-01	AW377898.1	EST_HUMAN	MFO-HT0208-221298-204-c08 HT0208 Homo sapiens cDNA
314	13118	25756	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25757	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25832	2.8	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
824	13594	26284	0.82	1.3E-01	X53330.1	NT	P.dumetii histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13765	26425	1.31	1.3E-01	AL117076.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Page 107 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1105	13862		2.6	1.3E-01	AL116265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1193	13945	26909	1.13	1.3E-01	AV712497.1	EST_HUMAN	AV712497 DCA Homo sapiens cDNA clone DCAAFF05 5'
1425	14172		1.18	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1850	14588	27303	0.97	1.3E-01	6680957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1952	14887	27400	2.18	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14896		1.22	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB8, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2288	16013		1.2	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2378	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome
2582	16306	28042	4.76	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cde
3065	15831	28474	1.01	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3443	16199	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3669	16718		1.43	1.3E-01	AL161681.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4137	16879		4.24	1.3E-01	AW384341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4145	16887	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2813895 3'
4257	16998	29827	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPDP Homo sapiens cDNA clone NPDAZE02 5'
4257	16998	29828	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPDP Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.78	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4497	17233	29863	2.68	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
4963	17688		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c06 TN0077 Homo sapiens cDNA
							h607608.x1 NCL_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2872879 3' similar to contains L1.b1 L1
5242	18048	30877	0.83	1.3E-01	AW465988.1	EST_HUMAN	L1 repetitive element;
5278	18083	30739	2.23	1.3E-01	AW804417.1	EST_HUMAN	QV0-UJ0093-100400-189-a06 UJ0093 Homo sapiens cDNA
5414	18213		0.77	1.3E-01	AF107793.1	NT	Emicella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5497	18295		0.75	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5638	18433	31346	0.97	1.3E-01	BF210920.1	EST_HUMAN	801874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5888	18881	31828	0.57	1.3E-01	BF627291.1	EST_HUMAN	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
5898	18881	31829	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6392	19161	32162	16.12	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6474	19241	32241	1.95	1.3E-01	X88891.1	NT	Cjacchus Intron 4 of visual pigment gene (red allele)
6691	19608		0.75	1.3E-01	W26367.1	EST_HUMAN	2813 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Page 108 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6914	19651		0.99	1.3E-01	BF528560.1	EST_HUMAN	602044345F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7162	19649		1.96	1.3E-01	H48964.1	EST_HUMAN	yf33d02.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:207076 5'
7859	20554		0.88	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890083 5'
7873	20568	33694	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
7902	20597	33727	1.17	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8136	20830		0.51	1.3E-01	BE562528.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8172	20868	33998	0.64	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8243	20937		4.47	1.3E-01	Z74102.1	NT	S cerevisiae chromosome IV reading frame ORF YDLO54c
8285	20979		4.44	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8426	21119	34258	1.02	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8847	21538	34683	0.58	1.3E-01	R11172.1	EST_HUMAN	yf39g11.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8847	21638	34684	0.58	1.3E-01	R11172.1	EST_HUMAN	yf39g11.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9119	21807	34973	0.61	1.3E-01	11088003	NT	Plutella xylostella granulovirus, complete genome
9119	21807	34974	0.61	1.3E-01	11088003	NT	Plutella xylostella granulovirus, complete genome
9372	21947	35120	3.71	1.3E-01	AF023128.1	NT	Oryctolagus cuniculus H+K+-ATPase alpha 2c subunit mRNA, complete cds
9671	22323		0.66	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9951	22589		0.99	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10030	22678	35894	0.85	1.3E-01	AWB51589.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10291	26128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36280	0.64	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10471	23117	36347	0.52	1.3E-01	AW247636.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10528	23225		2.93	1.3E-01	BF330699.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
10776	23458	36701	1.56	1.3E-01	H01883.1	EST_HUMAN	yf32d09.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11039	23710	36980	1.33	1.3E-01	AF118117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23879		3.28	1.3E-01	6871745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11304	23963	37263	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23963	37264	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37504	4.26	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11723	24317	37940	1.94	1.3E-01	BE616384.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
11755	24346	37878	1.44	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4300863 5'
12114	24607	31088	1.37	1.3E-01	BE618346.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'

Page 109 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12247	24695		4.43	1.3E-01	AJ242780.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
12274	24713		1.51	1.3E-01	Z13994.1	NT	R.norvegicus crp2 gene for cystatin related protein 2
12506	24915		1.43	1.3E-01	AB026829.1	NT	Ephydratia fluviatilis mRNA for sALK-6, complete cds
12836	24936		2.26	1.3E-01	AW001114.1	EST_HUMAN	WU24409.x1 Soares Dieckgraefe cdon, NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
374	13169	25944	8.42	1.2E-01	AI421744.1	EST_HUMAN	r39502.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_ma1 ANNEXIN V (HUMAN);
415	12828		1.05	1.2E-01	U68912.1	NT	Dichostellum discoideum ORF DG1016 gene, partial cds
534	13317		4.33	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1356	14103	28778	3.22	1.2E-01	U149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1355	14103	28778	3.22	1.2E-01	U149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1362	14110		4.36	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1498	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	el48e09.s1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1480584 3' similar to TR:Q16871 Q16871 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1627	14373	27062	1.26	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1646	14392	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	q68909.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1980553 3'
1762	14504		20.17	1.2E-01	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
1813	14650		1.03	1.2E-01	AW449368.1	EST_HUMAN	UI-H-B13-ak-e-10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734654 3'
2181	14910	27642	1.75	1.2E-01	BF248490.1	EST_HUMAN	601821667F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 5'
2284	15009	27748	1.2	1.2E-01	AI163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2597	15311	28047	1.49	1.2E-01	AW666566.1	EST_HUMAN	QV3-BND048-220300-12b-10 BN0046 Homo sapiens cDNA
							1a18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2847	15615	28262	1.3	1.2E-01	U18018.1	NT	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2903	15669	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	Human creatine kinase-B mRNA, complete cds
2935	15701	28350	2.92	1.2E-01	MT16394.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3004	15770	28418	0.87	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3224	15987	28641	1.59	1.2E-01	AW370668.1	EST_HUMAN	QV1-B70259-281099-021-c05 BT0259 Homo sapiens cDNA
3252	16014		1.12	1.2E-01	U87600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3472	16228		0.8	1.2E-01	Z59118.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2765131 to 3013540
3511	16267	28921	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

Page 110 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3511	16267	28922	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.48	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
4160	16900	29528	1.97	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4160	16900	29529	1.97	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4872	17408	30041	1.1	1.2E-01	Z48183.1	NT	L. esculentum mRNA for glyceralase-1
4739	17471		0.82	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5170	17979	30482	0.81	1.2E-01	AA74369.1	EST_HUMAN	ny63cd4.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282560 3'
5217	18025	30849	1	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5227	18034	30659	2.59	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5284	18089	30749	2.3	1.2E-01	Z98286.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5418	18217	30928	0.68	1.2E-01	Z48234.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.93	1.2E-01	BEG20945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898613 5'
6163	18930	31898	1.36	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6208	18981	31860	2.35	1.2E-01	AW845275.1	EST_HUMAN	ILO-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	M26825.1	NT	Mouse galactosyltransferase mRNA, complete cds
6337	19107	32087	0.67	1.2E-01	AA747535.1	EST_HUMAN	nx85cd1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6550	19315	32321	1.14	1.2E-01	BF347895.1	EST_HUMAN	602023112F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4158388 5'
6700	19816	32658	0.59	1.2E-01	AF298739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20488		1.4	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-409 BN0137 Homo sapiens cDNA
7882	20557	33683	4.36	1.2E-01	A0191753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7906	20601	33731	0.67	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8208	20902	34037	0.73	1.2E-01	A0832681.1	EST_HUMAN	NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8296	20989		10.29	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
8315	21008		3.34	1.2E-01	AF063772.1	NT	xc49cd07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:MI13452 LAMIN A (HUMAN);
8354	21047	34184	0.89	1.2E-01	J03956.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34186	0.89	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271736.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8599	21281		1.49	1.2E-01	U32714.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
						NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

Page 111 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8623	21315		0.62	1.2E-01	X15191.1	NT	Musculus DNA fragment of Apolipoprotein B gene
8471	22080	35252	2.93	1.2E-01	X77981.1	NT	S. cerevisiae HXT5 gene
9808	22555	35750	1.59	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cj Homo sapiens cDNA clone GUAKE08 5'
10811	23305	36543	1.38	1.2E-01	BF314481.1	EST_HUMAN	601600763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10801	23484		2.17	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10899	23672		3.18	1.2E-01	BE982324.2	EST_HUMAN	60165578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11084	23764		1.58	1.2E-01	BF314481.1	EST_HUMAN	601600763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF150493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11283	23944	37238	1.65	1.2E-01	RA40249.1	EST_HUMAN	yf80c02.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11492	24093		1.87	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11892	24462		2.53	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCIB12 3'
12230	24683		3.52	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD138 ANTIGEN)
12417	24798		3.16	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntablin gene, partial cds
12419	19317		3.19	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
12586	25384	30611	1.44	1.2E-01	BE081418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12610	24917	31007	5.86	1.2E-01	AI299903.1	EST_HUMAN	q20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	D98433	SWISSPROT	CYCLIN T
12663	24982	30989	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of the complete chromosome
12800	16228		1.81	1.2E-01	Z69118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
12812	25372	30614	1.38	1.2E-01	9845282	NT	Mus musculus protein (16kDa) similar to human SYK interacting protein (p16K), mRNA
551	13334	25964	0.8	1.1E-01	AI661003.1	EST_HUMAN	br18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
601	13378	26010	1.65	1.1E-01	AA559008.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb-X06985_rna1
1032	13792	26452	2.03	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	13921		1.3	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4288771 5'
1136	15561	26562	4.82	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1227	13977	26648	3.01	1.1E-01	D64004.1	NT	ESTT384142 MAGE resequences, MAGL Homo sapiens cDNA
1511	14257	28943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002965
2312	15037		1.85	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2540	15530		1	1.1E-01	6978678	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15288		1.17	1.1E-01	AW821809.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3030	15786	28442	0.82	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02.3'
3336	16096		1.76	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'
3444	16200	28850	1.21	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3570	16325	28972	0.77	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3698	16450	29089	1.47	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4080	16833	29456	1.28	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4090	16833	29457	1.28	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4226	16967		8.78	1.1E-01	AF157066.1	NT	Drosophila melanogaster Karschi protein (Klar) mRNA, complete cds
4254	16995	29624	0.77	1.1E-01	AW602058.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4594	17329	29956	0.96	1.1E-01	S44957.1	NT	Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4780	17612	30134	1.2	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
4967	18339		0.85	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
5077	17788	30412	1	1.1E-01	P70281	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18381		1.4	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5553	18448	31361	1.23	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5687	18480	31399	0.58	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537	31459	1.81	1.1E-01	X68851.1	NT	S.pombe sta8 gene encoding protein kinase
5781	18572	31500	5.31	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5936	18718	31676	1.67	1.1E-01	AJ007873.1	NT	Homo sapiens LGMD2B gene
5955	18737	31686	1.75	1.1E-01	BE769152.1	EST_HUMAN	PM3-F10024-130600-004-F12 F10024 Homo sapiens cDNA
5975	18757	31719	9.4	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0264-280899-011-a01 CT0264 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.25	1.1E-01	AF035748.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6381	19150	32149	0.72	1.1E-01	AI216307.1	EST_HUMAN	qg78406.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6612	19277	32278	3.71	1.1E-01	Q69835	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6804	18367		3.03	1.1E-01	AF032822.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

Page 113 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6697	19814	32655	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6948	19430	32445	0.7	1.1E-01	AE002153.1	NT	Ureaplasma urealyticum section 58 of 59 of the complete genome
6948	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7087	25423		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4060693 5'
7203	25107	32894	0.84	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (877)
7435	20112	33199	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.93	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7595	20263	33371	3.35	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
7888	20563	33690	0.5	1.1E-01	U67482.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8107	20801	33933	1.7	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20801	33934	1.7	1.1E-01	AA493574.1	EST_HUMAN	ih04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X91233.1	NT	ih04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8193	20887		1.14	1.1E-01	AW817818.1	EST_HUMAN	H.sapiens IL15 gene
8249	20943	34081	1.45	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-409 ST0270 Homo sapiens cDNA
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	DKFZp547P184.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P184 5'
8810	21602	34649	0.88	1.1E-01	A1807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8906	21597	34739	0.47	1.1E-01	AF050081.1	NT	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358818 3' similar to contains Alu repetitive element
8941	21632	34775	2.04	1.1E-01	AA192153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34776	2.04	1.1E-01	AA192153.1	EST_HUMAN	zp33b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
8933	21723	34877	0.74	1.1E-01	Y12727.1	NT	zp33b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9063	21762	34912	2.04	1.1E-01	T72876.1	EST_HUMAN	P. furiosus partial dph5 gene and argf gene
9090	21779		0.8	1.1E-01	BE683260.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb.M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9322	21989		0.88	1.1E-01	BE142305.1	EST_HUMAN	601496972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9306	22058		2	1.1E-01	BF085149.1	EST_HUMAN	GM3-HT0142-271099-028-g11 HT0142 Homo sapiens cDNA
9810	22461		0.5	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10017	22665		0.45	1.1E-01	BE315508.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10106	22754		1.57	1.1E-01	R80590.1	EST_HUMAN	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
10235	22893	36096	1.28	1.1E-01	U60529.1	NT	y99a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3'
10708	15796	28442	2.05	1.1E-01	F03265.1	EST_HUMAN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
							HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'

Page 114 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10840	23622		2.76	1.1E-01	AF169032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
10974	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	Y135F12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu repetitive element contains TAR1 repetitive element ;
10983	23658	36911	1.39	1.1E-01	6981361	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37079	1.68	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11169	23836	37117	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11169	23838	37118	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11277	23938	37230	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24268		1.65	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11690	24529		1.36	1.1E-01	AA192153.1	EST_HUMAN	z93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:927743 5'
12098	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-03 NT0112 Homo sapiens cDNA
12341	25160		1.97	1.1E-01	BE074556.1	EST_HUMAN	601680651R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'
12750	25012	30977	3.15	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4134085 5'
1179	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13998	26665	2.63	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:246577 3' similar to contains MER7.3
1371	14118	26794	1.85	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
2493	15210	27852	1.11	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3503	16269	28913	1.19	1.0E-01	BF033991.1	EST_HUMAN	UI-H-B13-alc-d-07-q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2739420 3'
3708	16461	29100	1.03	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3817	16569	29200	0.98	1.0E-01	AF297061.1	NT	601906499F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16569	29201	0.96	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	16685	29326	2.53	1.0E-01	BF369703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4518	17253		0.95	1.0E-01	A1792349.1	EST_HUMAN	QV2-NT0048-160800-318-605 NT0048 Homo sapiens cDNA
4694	17398	30032	1.19	1.0E-01	U60450.1	NT	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4896	17694	30217	2.35	1.0E-01	AW862344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5238	18044		9.73	1.0E-01	W86490.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5789	18590		1.21	1.0E-01	AK024472.1	NT	zh62h04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416685 3'
5934	18717	31675	14.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00085 protein, partial cds
6243	19017	31991	0.99	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6256	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	zu41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766259 3' similar to contains L1.13 L1 repetitive element ;
							zu67o12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'

Page 115 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924	19660		1.81	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131676 5' similar to contains Alu repetitive element;
7635	20300		2.67	1.0E-01	Y12488.1	NT	M.musculus vln gene
7709	20373	33486	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20528	33656	0.65	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.96	1.0E-01	AW189797.1	EST_HUMAN	xi09b01.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element ;
9094	21773	34937	1.04	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9395	22057	35228	0.51	1.0E-01	R44993.1	EST_HUMAN	yg33h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.6	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9450	22000		3.02	1.0E-01	AE007601.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9464	22074	35245	0.75	1.0E-01	W01955.1	EST_HUMAN	zc66c10.s1 Soares fetal heart_Nih-H19W Homo sapiens cDNA clone IMAGE:327282 3'
9721	22372	35571	1.67	1.0E-01	BF240154.1	EST_HUMAN	601905691F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST369615 IMAGE resequences, IMAGE Homo sapiens cDNA
10048	22696	35912					yh28a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72662 3' similar to contains Alu repetitive element
10228	22877	36089	0.89	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939098 5'
10534	23250		1.65	1.0E-01	AV159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10958	23694	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10968	23694	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23983	37283	5.22	1.0E-01	BE780543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
11510	24110		1.52	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) Inserted region, substrain:RIMD 0509852
11594	24193	37511	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for GLC-b chloride channel protein
11594	24193	37512	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for GLC-b chloride channel protein
11632	24416	37755	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLC9PG01 3'
11832	24416	37766	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLC9PG01 3'
12083	24921		4.32	1.0E-01	BE37719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3461833 6'
12300	24725		1.71	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

Page 116 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12317	24738		2.22	1.0E-01	X00954.1	NT	Drosophila melanogaster ftz gene
12814	24921		2.74	1.0E-01	BE537749.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3431833 5'
12877	25318		5.03	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25002		9.8	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15486	28224	1.27	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2780	15495	28235	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2780	15495	28236	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3260	16022	28871	1.32	9.9E-02	AF09810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
3833	16683	29324	0.75	9.9E-02	A1821837.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740932 3'
4832	17387	30003	0.93	9.9E-02	BE674249.1	EST_HUMAN	7477c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278988 3'
6875	17851	30547	9.17	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blestidin S deaminase, complete cds
7815	20510	33634	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
7815	20510	33635	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9166	21887	35055	0.98	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O. sativa RAMy3C gene for alpha-amylase
3100	15865		0.9	9.8E-02	4504578	NT	Homo sapiens I factor (complement) (IF) mRNA
3142	15908	28550	3.84	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4198	16339	29564	6.24	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4198	16339	29565	6.24	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7381	20061		0.77	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
8153	21884		1.18	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 28
11437	23204	36436	2.05	9.8E-02	BF037421.1	EST_HUMAN	601480793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
12052	24570		1.78	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1328	14077	26762	1.31	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1580	14926		1.49	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2257	14984	27724	2.08	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3865	16714		3.48	9.7E-02	Q98785	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18087	30895	0.94	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

Page 117 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5261	18067	30696	0.94	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5824	18708	31682	1.43	9.7E-02	AW054476.1	EST_HUMAN	EST366546 MAGC resequences, MAGC Homo sapiens cDNA
7198	19884	32958	3.24	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2987771 to 3213410
7882	20377	33705	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	AI953984.1	EST_HUMAN	wx78b08.x1 NCI_CGAP_Ox38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb.X52851_rna1
11152	23619		2.84	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligatin (Lgin) mRNA, partial cds
2009	14744	27470	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2009	14744	27471	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4311	17050	29675	5.9	9.6E-02	Z32686.2	NT	Protein mitralis fibrillar operon, strain HI4320
4840	17668	30276	0.99	9.6E-02	AW066230.1	EST_HUMAN	EST378303 MAGC resequences, MAGC Homo sapiens cDNA
6014	18795		3.13	9.6E-02	BE910039.1	EST_HUMAN	601488088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8274	20968		0.6	9.6E-02	AI137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
8444	22121	35300	1.31	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9772	22423		1.12	9.6E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
9939	22587	35790	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
9939	22587	35791	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22668	35884	0.5	9.6E-02	BF877270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250989 5'
10051	22899	35915	1.54	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-6 copy)
10061	22899	35916	1.54	9.6E-02	AB013986.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10158	22808	36024	3.35	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR (CD55)
10943	23334	36572	7.22	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
12852	24954		3.34	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
4081	16825	28452	2.1	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5579	18376	31289	0.85	9.5E-02	P51854	EST_HUMAN	ec68a09.s1 Stralagena fetal retina 937202 Homo sapiens cDNA clone IMAGE:887738 3'
6888	19881	32729	0.55	9.5E-02	AA780728.1	EST_HUMAN	Trimerurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7202	19888	32963	4.72	9.5E-02	AB003473.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7467	20141	33294	7.88	9.5E-02	AL161538.2	NT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7597	18376	31289	0.84	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7780	20476	33600	1.83	9.5E-02	BF036891.1	EST_HUMAN	601453842F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243 5'
7780	20475	33601	1.83	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10578	23273	36509	2.36	9.5E-02	BF035881.1	EST_HUMAN	601453842F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243 5'

Page 118 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10578	23273	36510	2.38	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1826	14564	27279	2.82	9.4E-02	BF671083.1	EST_HUMAN	602160882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291817 5'
1857	14595	27310	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14595	27311	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	16610	28249	4.43	9.4E-02	Z33059.1	NT	Macropodium DNA for CONTIG MC073
6225	18998	31976	0.63	9.4E-02	AF097363.1	NT	Trilicium aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8498	21180		2.48	9.4E-02	Z46963.1	NT	Acholeobacter sp. cysD, cobQ, cobQ, sodM, lysS, rubA, rubB, oxyR, ppk, migA, ORF2 and ORF3 genes
10851	20166	33288	2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and lpt35 gene, partial cds
11941	25255		1.76	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12671	24965		1.92	9.4E-02	AF198036.1	NT	Mycoplasma pulmonis hypothetical membrane protein P83 gene, complete cds
2988	15764		1.97	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3028	15792		6.32	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NIESG1), mRNA
3251	16013	28665	1.85	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	29502	3.51	9.3E-02	BE391943.1	EST_HUMAN	601266082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607663 5'
4132	16874	29503	3.51	9.3E-02	BE391943.1	EST_HUMAN	601266082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607663 5'
4685	17419		2.04	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5578	18373		0.87	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8148	20840	33972	0.62	9.3E-02	AW566007.1	EST_HUMAN	EST59 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9810	22263	35449	2.15	9.3E-02	BE982631.2	EST_HUMAN	601655988F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855981 3'
10091	22739	35953	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10091	22739	35954	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22868		3.6	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B1-afk-h-05-Q-UI-s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12194	25181		2.51	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12550	25209		8.43	9.3E-02	AW488850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_I_GBC_ST Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
12752	25254		2.1	9.3E-02	AF100956.1	NT	Molluscorum contagiosum virus subtype 1, complete genome
222	13034	25668	8.37	9.2E-02	U60315.1	NT	Molluscorum contagiosum virus subtype 1, complete genome
222	13034	25669	8.37	9.2E-02	U60315.1	NT	Molluscorum contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Molluscorum contagiosum virus subtype 1, complete genome
2224	14952		1.88	9.2E-02	R54156.1	EST_HUMAN	y9807.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3175	15938	28587	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16061	28709	0.85	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCL_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:328136 3'

Page 119 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3573	16328		1.28	9.2E-02	6765216	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4213	16954		0.99	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4274	17013		0.76	9.2E-02	BE209722.1	EST_HUMAN	600944385F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
7807	20602	33732	1.98	9.2E-02	T49920.1	EST_HUMAN	ya89c09.r1 Stratagene placenta (#937226) Homo sapiens cDNA clone IMAGE:88808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8076	20770	33899	2.2	9.2E-02	X95256.1	NT	H. vulgare xylose isomerase gene
11695	24290	37614	1.27	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
12736	25412		1.4	9.2E-02	11468872	NT	Podospira anserina mitochondrion, complete genome
414	12825	25439	4.19	9.1E-02	X77695.1	NT	O. cuniculus K12 keratin gene
4451	17187	28812	1.33	9.1E-02	AL101554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5843	18438	31352	1.44	9.1E-02	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and QLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7265	19968	33045	14.94	9.1E-02	AW160658.1	EST_HUMAN	au74605.YT Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7575	20244	33349	0.79	9.1E-02	AP000051.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7609	20275	33383	0.72	9.1E-02	U36073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
8822	21614	34659	0.88	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10327	22874		1.37	9.1E-02	T02894.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
10354	23001	36218	1.25	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Trifneustes gratillae=sea urchins, embryos, Genomic, 6276 nt]
10383	23028	36244	1.19	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12110	25348		1.4	9.1E-02	AA179901.1	EST_HUMAN	zp38f12.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12181	24653		2.12	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p56CDC gene, complete cds
12637	25204		1.93	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	13501	26155	4.3	9.0E-02	P16328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1631	14377	27064	5.28	9.0E-02	BE220482.1	EST_HUMAN	hiv39gt10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2808	15511	28252	6.45	9.0E-02	AF139522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2806	15511	28253	6.45	9.0E-02	AF139522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28744	0.84	9.0E-02	AF278135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4619	17354	28989	3.27	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5908	18891	31840	5.21	9.0E-02	W56037.1	EST_HUMAN	z689a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287684 5' similar to
6819	19381						PIR:S62171 S52171 small G protein - human ;
6868	19585	32619	1.14	9.0E-02	BF062651.1	EST_HUMAN	7h83d03.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Aliu
			0.72	9.0E-02	R02805.1	EST_HUMAN	repetitive element;
12486	24845						y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
1418	14166	26949	2.01	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (orf1), rOrf2 (orf2), EscR (escR), EscS (escS),
1418	14168	26950	1.99	8.9E-02	BF701593.1	EST_HUMAN	EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN
2386	16107	27848	1.22	8.9E-02	BE153572.1	EST_HUMAN	(escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
4176	16918		1.93	8.9E-02	AF286055.1	NT	602128030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
5760	18552	31474	3.22	8.9E-02	AW452122.1	EST_HUMAN	602128030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
5760	18552	31475	3.22	8.9E-02	AW452122.1	EST_HUMAN	PMD-HT0339-251189-003-d01 HT0338 Homo sapiens cDNA
5776	18587	31498	3.39	8.9E-02	11433478	NT	Altrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
7083	19782	32848	1.84	8.9E-02	P47259	SWISSPROT	UI-H-B13-alc-408-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
7458	20132		2.06	8.9E-02	Z79021.1	NT	UI-H-B13-alc-408-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
7949	20844	33768	1.08	8.9E-02	P29475	SWISSPROT	Homo sapiens similar to endoglycan (H. sapiens) (LOC683107), mRNA
8030	20726	33858	0.72	8.9E-02	BF701695.1	EST_HUMAN	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE
8030	20726	33859	0.72	8.9E-02	BF701695.1	EST_HUMAN	DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE ]
8406	21188	34331	4.72	8.9E-02	AA305319.1	EST_HUMAN	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA20F8
9520	22173	35358	0.8	8.9E-02	AI285627.1	EST_HUMAN	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
9520	22173	35357					(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
9632	22284	35477	0.76	8.9E-02	AA333358.1	EST_HUMAN	602128111F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
11882	25173		1.49	8.9E-02	P30143	SWISSPROT	602128111F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
11840	25207		1.48	8.9E-02	P19524	SWISSPROT	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
12085	24591		3.05	8.9E-02	BF696918.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1898980 3' similar to contains MER10.b1
12284	24716		1.61	8.9E-02	U29995.1	NT	MER10 repetitive element ;
1352	14100	26775	1.59	8.8E-02	Q27474	SWISSPROT	qu55c05.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1898980 3' similar to contains MER10.b1
3883	16033	29272	1.03	8.8E-02	AA295128.1	EST_HUMAN	MER10 repetitive element ;
							EST14454 Fetal brain I Homo sapiens cDNA 5' end
							EST14454 Fetal brain I Homo sapiens cDNA 5' end
							HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
							MYOSIN-2 ISOFORM
							602128682F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286180 5'
							Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
							PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
							EST11695 Uterus Homo sapiens cDNA 5' end

Page 121 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4214	16955		0.99	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8866	21577	34719	1.07	8.8E-02	AA151872.1	EST_HUMAN	zfp93a05.s1 Stratagene clone (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11228	23891	37178	6.92	8.8E-02	AL040128.1	EST_HUMAN	DKFZp434D1313.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
17806	24395	37729	1.49	8.8E-02	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24641	31098	2.66	8.8E-02	Z71551.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1642	14388	27077	1.15	8.7E-02	AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3681	16434	28077	3.66	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	16434	28078	3.66	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
6231	18037	30663	5.88	8.7E-02	AA286875.1	EST_HUMAN	z555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6231	18037	30664	5.88	8.7E-02	AA286875.1	EST_HUMAN	z555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32612	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6745	19578	32613	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6943	19425	32440	0.71	8.7E-02	AF281342.1	NT	Oncofynchus mykiss TAT-binding protein 1 mRNA, partial cds
7781	20457		0.45	8.7E-02	AA284532.1	EST_HUMAN	z20e03.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:713692 3'
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10610	23304		2.46	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11282	23943	37237	2.55	8.7E-02	AJ007763.1	NT	Glucobacter oxydans rRNA-16S and rRNA-16S genes
12145	24833		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	6678057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1230	19879	26849	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudocautosomal region; segment 2/2
2240	14868	27706	1.82	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3183	15946	28596	4.57	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds

Page 122 of 536  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3636	16388		3.77	8.0E-02	AF163362.1	NT	Dictyostelium discoidium adenyl cyclase (acrA) gene, complete cds
5134	17852		0.88	8.0E-02	BF070298.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
6003	18784	31746	4.75	8.0E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6281	19054	32033	1.56	8.0E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q82, mu switch region (part a)
6281	19054	32034	1.58	8.0E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q82, mu switch region (part a)
7481	20153	33248	1.34	8.0E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7831	20626	33651	1.25	8.0E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
7831	20626	33652	1.25	8.0E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
7899	20664	33788	0.62	8.0E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11008), mRNA
8031	20728		0.81	8.0E-02	U60168.1	NT	Dictyostelium discoidium proteasome subunit C2 homolog PrC (prC) gene, complete cds
9637	22289	35482	1.76	8.0E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9673	22325		0.58	8.0E-02	AW562153.1	EST_HUMAN	h20c08.x1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872846 3'
10063	22701	35918	0.81	8.0E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1204 mRNA, complete cds
10855	23545	36792	1.8	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10855	23545	36793	1.8	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	23877	37183	4.64	8.0E-02	BF305006.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11214	23877	37184	4.64	8.0E-02	BF305006.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11417	23184	36414	5.97	8.0E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11588	24187	37481	2.11	8.0E-02	AF283680.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.0E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.0E-02	AA885491.1	EST_HUMAN	α483b07.s1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA
5621	18417		1.28	8.0E-02	P08089	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5921	18708	31658	0.95	8.0E-02	AF233985.1	NT	M PROTEIN, SEROTYPE 6 PRECURSOR
8504	21196	34340	1.65	8.0E-02	6754779	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
9736	22387	35591	2.81	8.0E-02	BE833054.1	EST_HUMAN	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35592	2.81	8.0E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10281	22909	36119	0.54	8.0E-02	X76731.1	NT	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10382	23028	36243	0.87	8.0E-02	11418108	NT	V. armodytes gene for armodytoxin C
11105	23775		8.87	8.0E-02	AF155510.1	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11125	23794	37070	4.43	8.0E-02	AB001562.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
						NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12700	24981		3.8	8.4E-02	AA362834.1	EST_HUMAN	EST172736 Ovary II Homo sapiens cDNA 6' and
2672	16602	28121	3.73	8.4E-02	W69330.1	EST_HUMAN	z444e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:349532 5'
3801	16553	29184	1	8.4E-02	A1827586.1	EST_HUMAN	wf10f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSR1 repetitive element;
4321	17080	29686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4321	17080	29686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042656.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5229	18035	30681	9.84	8.4E-02	BE287153.1	EST_HUMAN	601190439F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6590	18353	32366	1.72	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7928	20623	33761	7.18	8.4E-02	BE086074.1	EST_HUMAN	CM3-BT0760-260-400-162-d05 BT0760 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10280	22908	36118	1.83	8.4E-02	A1735184.1	EST_HUMAN	as88g10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
12070	24594	31122	1.68	8.4E-02	R75408.1	EST_HUMAN	O88312 GOB-4.;
2005	14741	27465	0.92	8.3E-02	5835680	NT	y83h12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27468	0.92	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3680	16335	28980	6.91	8.3E-02	P75334	SWISSPROT	Ixodes hexagonus mitochondrion, complete genome
3607	16360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3607	16360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6166	18943	31814	1.05	8.3E-02	A1942338.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6273	19046	32023	3.05	8.3E-02	AF052683.1	NT	wo78f11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
7880	20575	33702	2.98	8.3E-02	AF185787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7911	20606		1.46	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drip2) mRNA, complete cds
8198	20892		1.32	8.3E-02	AA867873.1	EST_HUMAN	cg88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.1 L1 L1
9438	22116	35291	1.41	8.3E-02	AW583503.1	EST_HUMAN	replicative element;
9451	22001		1.88	8.3E-02	AI161595.2	EST_HUMAN	oq81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
10240	22898		0.49	8.3E-02	AF020409.1	NT	la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
12158	26353		1.67	8.3E-02	BE68458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE ;
1357	14105		7.15	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1481	14228	26814	1.88	8.2E-02	AF167077.2	NT	Dicotyledon discoidium DocA (docA) mRNA, complete cds
3071	15837		2.07	8.2E-02	AL163206.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928993 5'
3784	16336		1.35	8.2E-02	AL161498.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
						NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
						NT	Homo sapiens chromosome 21 segment HS21C006
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

Page 124 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3989	16737	29371	1.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4231	16992	29617	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16992	29618	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16992	29619	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5070	17789		2.39	8.2E-02	Z69893.1	NT	T.inflatum transposon Restless DNA
5252	18068	30687	1.49	8.2E-02	BE97030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	19681	32707	3.09	8.2E-02	AF308555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20298		0.67	8.2E-02	AV74334.1	EST_HUMAN	AV74334.1 CS Homo sapiens cDNA clone CBLANF07 5'
8870	21362	34509	2.95	8.2E-02	AW875128.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
9499	22152	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9663	22315	35512	2.24	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355586 5'
12164	24648	31102	4.03	8.2E-02	AE002246.2	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
12554	25138		3.65	8.2E-02	AF275366.1	NT	Xyella fastidiosa, section 152 of 229 of the complete genome
5688	18463	31378	0.79	8.1E-02	AE004006.1	NT	A1484F Heart Homo sapiens cDNA clone A1484
6286	18059	32040	1.19	8.1E-02	T11532.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7087	19786		0.68	8.1E-02	AL163279.2	NT	wd86f08.xt NCJ CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
7482	20154		1.26	8.1E-02	AI692881.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20932	34067	0.61	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20932	34068	0.61	8.1E-02	11428974	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
9812	22463		1.64	8.1E-02	AY006150.1	NT	Homo sapiens chromosome 21 segment HS21C002
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	EST366723 MAGE resequences, MAGEC Homo sapiens cDNA
6	16534	25447	5.03	8.0E-02	AW854653.1	EST_HUMAN	Mollusca contagiosum virus subtype 1, complete genome
916	13682	26344	0.79	8.0E-02	U60315.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1694	15576	27134	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1694	15576	27135	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1898	14633	27343	3.27	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2374	15096	27835	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8903 complete genome, 17127, 2137259-2287269
2374	15096	27836	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8903 complete genome, 17127, 2137259-2287269
2473	15181		4.2	8.0E-02	BE246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076619 5'
2823	13827	26486	0.98	8.0E-02	M23449.1	NT	Diktyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2901	15687	28315	1.45	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3797	16549	29182	1.01	8.0E-02	AW988118.1	EST_HUMAN	EST378181 MAGE resequences, MAGI Homo sapiens cDNA

Page 125 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4725	17457	30063	1.43	8.0E-02	AI434202.1	EST_HUMAN	i31902.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2132114.3'
4764	17498		6.33	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5108	17826	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	U1-H-B1-af04-10-0.U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721647.3'
5801	18591	31516	3.16	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18691	31516	1.82	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114893.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9289	21956	35127	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9289	21956	35128	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10058	22706		0.55	8.0E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
10692	23383	36623	2.27	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12185	24665	31070	6.39	8.0E-02	AJ005375.1	NT	Drosophila orena hunchback region
12748	17903		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.6E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959810.5'
2978	15744	28392	7.25	7.9E-02	AI582029.1	EST_HUMAN	ar68c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173648.3' similar to gb:Z26876.60S RIBOSOMAL PROTEIN L38 (HUMAN);
3777	16529	29168	0.97	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3832	16583	29217	5.01	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	16583	29218	5.01	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4845	17378	30011	0.99	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156401.5'
4760	17492		1.31	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4851	17581	30204	1.02	7.9E-02	L24757.1	NT	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
6597	19360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
7831	20826	33754	2.79	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smk4p (SMT4) gene, complete cds
9827	22576	35773	4.21	7.8E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465.3' similar to WP:C37A2.2 CE08611;
9827	22576	35774	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465.3' similar to WP:C37A2.2 CE08611;
1188	13940	26804	1.77	7.8E-02	AI793275.1	EST_HUMAN	ou63b02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467.5' similar to contains L1:13 L1 repetitive element;
1188	13940	26805	1.77	7.8E-02	AI793275.1	EST_HUMAN	ou63b02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467.5' similar to contains L1:13 L1 repetitive element;

Page 126 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
6976	19467	32479	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6976	19457	32480	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8684	21376	34520	0.71	7.8E-02	BE897847.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8778	21471	34816	0.66	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
8951	21642	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21642	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8261	22016	36183	1.07	7.8E-02	AA469364.1	EST_HUMAN	nc88806.r1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:774731
9701	22352	35547	0.62	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3899281 to 4214814
10562	23258	36494	4.58	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12764	25016		3.92	7.8E-02	AF096349.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1378	15568	28800	1.25	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	16329		1.97	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5456	18255	31145	0.59	7.7E-02	AF062836.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33825	5.37	7.7E-02	AA402948.1	EST_HUMAN	TR:G1173805 G1173905 SPLICOSOME ASSOCIATED PROTEIN. ;
9735	22386	35580	3.94	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10031	22879	35995	0.85	7.7E-02	AJ318662.1	EST_HUMAN	la80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
10031	22879	35996	0.85	7.7E-02	AJ318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10933	23613	36963	4.51	7.7E-02	11422757	NT	la80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
12389	25215		2.68	7.7E-02	11436859	NT	Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
3382	16141	28798	1.97	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3403	16161	28812	1.14	7.6E-02	AA296447.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3547	16302	28952	0.71	7.6E-02	AJ400877.1	NT	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protobaccharin 43
6006	18787	31749	0.81	7.6E-02	AJ051275.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
							an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'

Page 127 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6263	19037	32012	0.92	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9797	22448		1.63	7.6E-02	AL130078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
10119	22767	35979	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d08 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE659638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10487	23133	36369	0.71	7.6E-02	X92656.1	NT	L. esculentum mRNA for those phosphate translocator
10487	23133	36360	0.71	7.6E-02	X92656.1	NT	L. esculentum mRNA for those phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW996845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
767	13540	26199	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	26200	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	AJ948714.1	EST_HUMAN	wq24h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8236	20930	34066	1.05	7.5E-02	AJ864387.1	EST_HUMAN	wf62502.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:U14328 ALPHA
8406	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
8932	22580		0.64	7.6E-02	BF221730.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10390	23036	36252	0.7	7.5E-02	BF206809.1	EST_HUMAN	7661c05.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10488	23134	36361	0.72	7.5E-02	X79460.1	NT	MER27 repetitive element;
466	13260	25891	1.46	7.4E-02	AW838547.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1445	14192		0.92	7.4E-02	AF030027.1	NT	G.fini DSM 20113 16S rDNA
2585	16299		1.32	7.4E-02	6755069	NT	RCS-L T0054-260100-011-H09 L70054 Homo sapiens cDNA
3581	16336	28981	0.86	7.4E-02	AJ807895.1	EST_HUMAN	Equine herpesvirus 4 strain NS80587, complete genome
4656	17390	30024	2.03	7.4E-02	L78810.1	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4741	17473	30108	2.94	7.4E-02		NT	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4889	17616	30235	2.1	7.4E-02		NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
6403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	Rattus norvegicus ActinVn receptor like kinase 1 (Acvrl1), mRNA
7801	20496	33618	1.52	7.4E-02	BE880112.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchbp), mRNA
8399	21092	34228	1.03	7.4E-02	U56039.1	NT	Yg14g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
8064	21793	34913	1.12	7.4E-02	AW628605.1	EST_HUMAN	601493386F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895284 5'
							Human perlecan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
							fh97df11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987891 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9094	21753	34914	1.12	7.4E-02	AW628605.1	EST_HUMAN	h67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9339	20410	33525	0.52	7.4E-02	A1672938.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9339	20410	33526	0.52	7.4E-02	A1672938.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9714	22365	35563	1.03	7.4E-02	U62293.1	NT	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9841	22492	35692	0.52	7.4E-02	BF512678.1	EST_HUMAN	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10939	23619	36869	1.26	7.4E-02	AA059167.1	EST_HUMAN	UI-H-BW.1-ang-g-06-0-JJ.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
12128	24618		1.53	7.4E-02	11525863	NT	zif4e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:391720 5'
12381	25329		2.21	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
466	13242	25881	1.5	7.3E-02	BE984961.2	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
458	13242	25882	1.5	7.3E-02	BE984961.2	EST_HUMAN	601668738R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886209 3'
669	13445	26095	3.9	7.3E-02	AEC01789.1	NT	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1484	15570	26900	3.62	7.3E-02	AW900281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1837	15580		12.41	7.3E-02	AL163302.2	NT	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
6361	19131	32126	1.32	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7368	20048	33129	2.58	7.3E-02	P05143	SWISSPROT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
8088	20762		1.15	7.3E-02	7662107	NT	PROLINE-RICH PROTEIN MP-3
9110	21798		1.14	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11179	19131	32126	2.06	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
11844	24428		5.07	7.3E-02	11560138	NT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
117	12937	25577	1	7.2E-02	AE000892.1	NT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
117	12937	25578	1	7.2E-02	AE000892.1	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC84171), mRNA
1458	14205	26890	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
1458	14205	26891	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
2652	15267		2.83	7.2E-02	U14794.1	NT	Homo sapiens chromosome 21 segment HS21C101
3865	16615	29254	0.85	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
4312	17051	29878	4.65	7.2E-02	BF572307.1	EST_HUMAN	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
4844	17378	30010	0.7	7.2E-02	11466563	NT	UI-H-BW0-ajl-a-05-Q-JJ.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
							602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
							Rhodomonas salina mitochondrion, complete genome

Page 129 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6205	18013	30635	2.88	7.2E-02	U87531.1	NT	Methanococcus jannaschii section 73 of 160 of the complete genome
6206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8087	20781	33910	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8962	21653		0.61	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22164	35346	2.32	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAU001 5'
9859	22311	35509	3.8	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35667	0.93	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028436 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	hq2411.1 NCI CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10092	22740	35955	0.62	7.2E-02	AA769204.1	EST_HUMAN	oa62c07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10260	22898	36108	1.93	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	5.64	7.2E-02	BE5685003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10395	23041		3.68	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451569 5'
10509	23155	36381	0.48	7.2E-02	AA708897.1	EST_HUMAN	z28h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10630	23512	36753	3.3	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY009090.1	NT	Homo sapiens putative transmembrane protein dectin-1 mRNA, complete cds
12035	24560	31113	1.67	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12089	24563		4.45	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seraniki P) Homo sapiens cDNA clone PS13D5 3'
12182	24654		1.73	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12198	25185		8.19	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12699	25362		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1897	14634	27344	2.01	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2260	15015	27751	5.07	7.1E-02	BF208902.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4092881 6'
7807	20502	33622	0.77	7.1E-02	AI125264.1	EST_HUMAN	qd92a10.xt Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11922	24483		6.41	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13289	25931	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14233		1.27	7.0E-02	X98877.1	NT	Martellia Mcut-1 gene
1766	14498	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	Z66804.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:509568 3'
3027	15793	28440	2.1	7.0E-02	AW138152.1	EST_HUMAN	U1-H-B11-acyc-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
							af65a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
3878	16628	28266	0.74	7.0E-02	AA815438.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4119	16681		1.26	7.0E-02	AW792982.1	EST_HUMAN	CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4189	16930	29560	1.06	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4877	17604	30227	7.24	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5293	18098		0.57	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7300	18983	33059	1.29	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GK Homo sapiens cDNA clone GKCCAE08 5'
7508	20177	33271	0.84	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial azorin, XL spliced variant (acz gene)
8998	21698	34836	1.26	7.0E-02	9628113	NT	African swine fever virus, complete genome
9497	22150	35331	1.24	7.0E-02	K02801.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
9852	22502	35702	0.51	7.0E-02	U27266.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11345	24035	37338	4.88	7.0E-02	AA724295.1	EST_HUMAN	ah89a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507888	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	16525	29163	1.41	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3773	16525	29164	1.41	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucoside specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	601192383F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536253 5'
5127	17845	30462	1.25	6.9E-02	BE264605.1	EST_HUMAN	Canine distemper virus strain A7517, complete genome
7516	20187		0.61	6.9E-02	AF164967.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
7981	20846		1.12	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8451	21143	34282	1.01	6.9E-02	BE667435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883030 5'
8451	21143	34293	1.01	6.9E-02	BE667435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883030 5'
9018	21708	34860	0.7	6.9E-02	U22867.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12085	24580		1.82	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein

Page 131 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12332	24685		1.69	6.8E-02	P46821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
12447	24817		1.46	6.9E-02	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1876	14613	27321	1.56	6.8E-02	AA496759.1	EST_HUMAN	aa30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1875	14613	27322	1.56	6.8E-02	AA496759.1	EST_HUMAN	aa30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
3097	15862	28503	1.19	6.8E-02	AA781896.1	EST_HUMAN	af75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
3097	15862	28504	1.19	6.8E-02	AA781896.1	EST_HUMAN	af75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
3097	15862	28505	1.19	6.8E-02	AA781896.1	EST_HUMAN	af75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3'
4518	17251		0.86	6.8E-02	BE141076.1	EST_HUMAN	MRO-H10089-071098-001-c05 HT0069 Homo sapiens cDNA
6525	19291		0.6	6.8E-02	P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
6789	19460		1.09	6.8E-02	BE061890.1	EST_HUMAN	RC1-B10264-090300-017-409 BT0254 Homo sapiens cDNA
7180	19868	32939	8.73	6.8E-02	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C038
7584	20252	33358	0.63	6.8E-02	U18956.1	NT	Dicystostellum discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8186	20880	34017	5.01	6.8E-02	A1248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8186	20880	34018	5.01	6.8E-02	A1248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11873	26379		2.3	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12001	24637		2.85	6.8E-02	AA766014.1	EST_HUMAN	ah67f06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12551	24888		1.65	6.8E-02	AW975839.1	EST_HUMAN	EST387948 IMAGE resequences, MAGN Homo sapiens cDNA
12613	24920		3.06	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1519	14268		1.93	6.7E-02	AF116536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1'01 allele, complete cds
1886	14923	27333	2.27	6.7E-02	AI220285.1	EST_HUMAN	qg78c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3706	16459	26097	4.52	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
7749	20446	33667	0.55	6.7E-02	X62695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7749	20446	33668	0.55	6.7E-02	X62695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8337	21030	34167	0.47	6.7E-02	AW082688.1	EST_HUMAN	xb67c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
8500	22153	35333	0.69	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9500	22153	35334	0.69	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1348	14096	26771	1.07	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2180	14909	27641	3.31	6.6E-02	A1289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3456	16212	28865	10.57	6.6E-02	R64306.1	EST_HUMAN	yf18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3471	16227	28881	2.69	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3471	16227	28882	2.59	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4080	16805	28436	1.29	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4921	17849	30281	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17849	30282	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6489	19256	32258	3.44	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6701	19283	32286	0.58	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.58	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20542	33670	1.81	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21085	34206	0.84	6.6E-02	AF06055.1	NT	Dictyostelium discoideum darlin (dar1) gene, complete cds
8878	21370		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8879	21511	34654	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8819	21511	34655	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8851	22501	35701	0.65	6.6E-02	A1458752.1	EST_HUMAN	997g06.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149493.3
8987	22836	35846	1.68	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
10022	22870		0.63	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10883	23563	36811	6.88	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-008-a12 SN0064 Homo sapiens cDNA
11887	24451	37793	1.48	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.66	6.6E-02	9937891	NT	Mus musculus DIPB gene (Dipb), mRNA
12740	25006		1.38	6.6E-02	AF187430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	26977	2.49	6.6E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:39854178.6
968	13732	26398	1.32	6.6E-02	7708068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26793	3.08	6.6E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27189	1.77	6.6E-02	AE000784.1	NT	Aquifex aeolicus section 98 of 109 of the complete genome
5471	18270	31162	2.03	6.6E-02	AA443891.1	EST_HUMAN	z46h12.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:756743.3' similar to gb:M26038
6877	17953	30549	0.85	6.6E-02	U22681.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
9842	22493	35693	0.55	6.6E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds
9842	22493	35694	0.55	6.6E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3885637.3'
10363	23010	36225	0.48	6.6E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3885637.3'
10636	23232	36486	5.68	6.6E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138.5'
11894	24483		3.73	6.6E-02	M21496.1	NT	z32g05.g1 Soares NIH-MP1 S1 Homo sapiens cDNA clone IMAGE:665144.3'
12240	24691		4.66	6.6E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
661	13343	25970	2.09	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
3014	15780	28429	0.96	6.4E-02	6996923	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
4839	15780	28429	1.18	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

Page 133 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5363	18186	30850	1.67	6.4E-02	A1191986.1	EST_HUMAN	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR repetitive element;
5781	18582	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31763	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1.4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31784	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1.4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6308	19080	32065	0.62	6.4E-02	AF1672898.1	EST_HUMAN	we73g12.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3'
6719	19634	32677	6.43	6.4E-02	BE874448.1	EST_HUMAN	601680425R2 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:3850609 3'
7360	20041	33119	0.84	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeat) (Cct6a), mRNA
8563	21255	34392	3.42	6.4E-02	AA083005.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8025	21715	34868	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9486	22139		0.55	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g08 OT0083 Homo sapiens cDNA
9817	22270	35457	1.73	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37629	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12188	24659	31065	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3590	16344		2.38	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6045	18825	31786	1.18	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087499 5'
7142	19829		0.82	6.3E-02	X97899.1	NT	Hi sapiens gene encoding La autoantigen
9191	21861	35026	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
9913	22562	35758	2.64	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10171	22819		0.85	6.3E-02	AV898070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10615	18825	31786	2.96	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087499 5'
4224	16965	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

Page 134 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4304	17043		1.02	0.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		6.31	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (ROB2)
6698	19816	32656	0.65	6.2E-02	D46530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7627	20198	33292	1.03	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8846	25429		0.8	6.2E-02	M81101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35092	0.52	6.2E-02	AA78450.1	EST_HUMAN	af20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9380	22042	35214	1.65	6.2E-02	6677898	NT	Mus musculus striatal cell derived factor receptor 2 (Sdfr2), mRNA
11095	23765	37039	1.56	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyl gene)
11885	24449	37791	1.74	6.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uggf) mRNA, complete cds
11889	25405		13.39	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.2E-02	BF112039.1	EST_HUMAN	737h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523816 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
249	13058	25697	5.59	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3972	16721		2.29	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
6023	18903		1.4	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33988	3.76	6.1E-02	X69268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8559	21251	34398	0.57	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:3934604 3'
8559	21251	34399	0.57	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10630	23823	36560	4.91	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
11862	24446	37787	1.27	6.1E-02	AB025333.1	NT	Epiplatys burgeni mRNA for RNA polymerase III largest subunit, partial cds
11945	25323		2.27	6.1E-02	X70989.1	NT	S. japonicum mRNA for serine-enzyme
12633	24933		5.61	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
98	12922	25569	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
98	12922	25569	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
1239	13988	26855	1.54	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 138 of the complete genome
2692	15391	28130	1.09	6.0E-02	AW68848.1	EST_HUMAN	EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA
							Mesocricetus cordi mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2775	15480		1.62	6.0E-02	AB031289.1	NT	ATPase subunit 6, and NADH dehydrogenase subunit 2
2937	12922	25559	0.8	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2937	12922	25560	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Striatogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

Page 135 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	15986	28639	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15986	28840	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE984443.2	EST_HUMAN	601868150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5037	17756	30370	0.69	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW37021.1	EST_HUMAN	RC3-BT0263-011189-013-504 BT0263 Homo sapiens cDNA
6122	18900	31888		6.0E-02	AI807637.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element;
6891	17967	30524	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA
6891	17967	30525	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA
7088	19777	32842	2.33	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7580	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf58h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764189 3'
8321	21014		0.54	6.0E-02	11466495	NT	Rec114h08a amaranth mitochondrion, complete genome
9172	21842	36007	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	36008	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9308	21973	35147	1.88	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
9308	21973	35148	1.68	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
11306	23965		1.69	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X89181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31084	2.16	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12584	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
223	13036	25671	3.87	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN;
2982	15748	28396	2.89	6.9E-02	AF190289.1	NT	RC1-DT0001-280100-012-a10 DT0001 Homo sapiens cDNA
4817	17548	30173	1	5.9E-02	AF006304.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5123	17841	30457	0.73	5.9E-02	AW028748.1	EST_HUMAN	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17841	30458	0.73	5.9E-02	AW028748.1	EST_HUMAN	wf34e02.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:2531460 3' similar to TR:O65386
8515	21207	34350	1.68	5.9E-02	9055249	NT	O65386 F12F1.20 PROTEIN;
9351	20422		0.8	5.9E-02	BF242748.1	EST_HUMAN	wf34e02.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							Mus musculus trophoblast related homeobox 5 (Drosophila) (trx5), mRNA
							601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105694 5'

Page 136 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23378		3.2	5.8E-02	6678870	NT	Mus musculus follistatin-like (Fstl), mRNA
10944	23623	36872	1.44	5.8E-02	11433356	NT	Homo sapiens nleln (LOC51199), mRNA
11544	24144		1.59	5.8E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
912	13678		5.18	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2884	15632		0.86	5.8E-02	AJ223821.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
4322	17061	29687	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17061	29688	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	AJ247505.1	EST_HUMAN	qh5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4510	17245	29880	4.95	5.8E-02	AJ247505.1	EST_HUMAN	qh5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33352	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8565	21257	34394	0.87	5.8E-02	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12084	24580		1.79	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25398		7.06	5.8E-02	AA604288.1	EST_HUMAN	no75611.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3053	15919	28463	1.39	6.7E-02	AI081644.1	EST_HUMAN	ou83b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632485 3' similar to WP:C37A2.2
3088	16834	28478	1.29	5.7E-02	AF119117.1	NT	CE08811;
3694	16448		0.97	6.7E-02	AF001292.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3783	16535	29173	2.45	5.7E-02	AW968791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13R1), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
4637	17371		1.01	5.7E-02	M95099.1	NT	EST1378865 MAGE resequences, MAGI Homo sapiens cDNA
7438	20115	33203	0.89	5.7E-02	D78003.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7438	20115	33204	0.89	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8055	20749	33880	1.42	5.7E-02	AJ296090.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
9760	22401	35608	0.84	5.7E-02	6681260	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
				5.7E-02		NT	Mus musculus ect2 oncogene (Ect2), mRNA
11143	23810	37090	4.42	5.7E-02	AI762885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11143	23810	37091	4.42	5.7E-02	AI762885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11321	24012		1.59	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12285	26213		7.24	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds

Page 137 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12516	25283		3.18	5.7E-02	AF217490.1	NT	Homo sapiens (fragile 16D) oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12650	25397		2.61	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1518	14266	26951	1.57	5.6E-02	AF094455.1	NT	Hydrocotyle reticulifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4595	17330	29957	1.12	5.6E-02	AB013100.1	NT	Lycopodium obscurum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4648	17382	30014	1.46	5.6E-02	AA280599.1	EST_HUMAN	z645c01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6562	19327	32334	6.57	5.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN.;
6791	18535	32563	1.25	5.6E-02	AA869182.1	EST_HUMAN	cd4741.2.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element contains element L1 repetitive element;
7051	19742	32804	3.05	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
7063	19764	32819	0.69	5.6E-02	AI983738.1	EST_HUMAN	w23405.x1 NCL CGAP_Bn53 Homo sapiens cDNA clone IMAGE:2559869 3' similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20388	33502	0.68	5.6E-02	AI83583.1	EST_HUMAN	q644g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1794308 3'
8701	21393	34639	2.88	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463279 5'
8701	21393	34640	2.88	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463279 5'
9712	22363	35581	1.09	5.6E-02	AA482864.1	EST_HUMAN	n48d07.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;
11556	24155		2.35	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2660	15370	28108	6.8	5.5E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3209	16972	28625	3.93	5.5E-02		NT	Mus musculus SF3 domain protein 1B (SF3d1B), mRNA
4191	16932	29581	1	5.5E-02	L41561.1	NT	Galid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5935	18370	31281	3.58	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	18991	33038	2	5.5E-02	6755902	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8019	20714	33845	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
8019	20714	33846	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
9565	22208	35392	0.6	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9565	22208	35393	0.6	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9850	22302	35497	1.32	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10943	23622	36871	7.28	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cia) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB).>

Page 138 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12787	25349	30604	1.49	5.6E-02	11421332	NT	Homo sapiens hypothetical protein S1RP-b2 (S1RP-b2), mRNA
3019	15785		0.91	5.4E-02	AJ277488.1	NT	Oryza sativa tbb3-1 gene for putative Bowman Birk trypsin inhibitor
3416	17885		5.78	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3891	16641	28281	0.76	5.4E-02	U96806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z99118.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2613730
8969	21659	34809	0.55	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10637	23234	36467	1.62	6.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37078	1.32	6.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA
1031	13791	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1031	13791	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1495	14242	26929	14.72	5.3E-02	T94759.1	EST_HUMAN	ye37f12.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01506
2501	15218	27961	2.47	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2843	15709	28360	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tggS gene
2843	15709	28361	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster larminin B2 gene, complete cds
3150	15913	28558	5.51	5.3E-02	AJ276408.1	NT	Drosophila melanogaster larminin B2 gene, complete cds
5029	17749	30361	6.34	5.3E-02	M80463.1	NT	Pseudomonas putida tggS gene
5236	18042	30670	1.98	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
6236	18042	30671	1.98	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6785	18629	32556	5.01	5.3E-02	9695413	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6992	19685	32733	1	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7260	19944		2.06	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7777	20399	33514	0.65	5.3E-02	P38742	SW/ISSPROT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8304	20998		0.7	5.3E-02	U10098.1	NT	HYPOTHEICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
9023	21713	34867	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cystatin C (cstC) gene, complete cds
10032	22680	35897	0.62	5.3E-02	AB022605.1	NT	Podospira anserina mitochondrial epsilon-sen DNA
10032	22680	35898	0.62	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7)methyltransferase, complete cds
							Homo sapiens hCMT1b mRNA for mRNA (guanine-7)methyltransferase, complete cds
10156	22804		0.63	5.3E-02	Y07807.1	NT	D.reio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postembryogenesis, 20-28 hpf)
10230	22878	36090	0.7	5.3E-02	X68432.1	NT	B.reio pou[c] mRNA for transcription factor

Page 139 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12776	25030	30894	1.43	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		160.56	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEPTA) mRNA
3112	15877	28516	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	15877	28517	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16669	29310	1.23	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
3921	16671		1.19	5.2E-02	6671757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4245	16988	29609	3.02	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nrr-1 mRNA, complete cds
5053	17772		0.9	5.2E-02	AA297940.1	EST_HUMAN	EST11352 Uterus Homo sapiens cDNA 5' end
5928	18617	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AB30965.1	EST_HUMAN	w80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element:
7174	19860	32932	3.13	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8085	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9829	22282	35472	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9829	22282	35473	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24795		1.93	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2364	16086		1.17	6.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 5477 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4178	16918	29547	1.03	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4950	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6576	19339	32360	0.72	6.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6760	17929	30584	1.44	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8161	20845	33975	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8151	20845	33976	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8245	20839	34076	1.48	5.1E-02	AJ131666.1	NT	Spodoptera littoralis mRNA for 3-dehydrocyclohexene 3beta-reductase
8783	21475	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8783	21476	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9709	22360	35556	6.2	6.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.89	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10733	23420	36681	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	36682	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AF193076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
12421	24797		2.56	5.1E-02	AF082467.1	NT	Cucumis melo polygalacturonase precursor (MFG3) mRNA, complete cds

Page 140 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12878	24968		1.41	5.1E-02	AA534104.1	EST_HUMAN	nt73102.s1 NCL CGAP_P10 Homo sapiens cDNA clone IMAGE:988139
470	13268	25894	1.84	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	26599	6.54	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1883	14719	27438	3.91	5.0E-02	P02810	SWISSPROT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-4/PIF-5) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	26397	1.28	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7306610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (ULK2), mRNA
3682	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3672	16425	28086	5.83	5.0E-02	U12769.2	NT	Anthrax pernyi period clock protein homolog mRNA, complete cds
4770	17502		0.99	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18819	31780	0.85	5.0E-02	AF098294.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6218	18990		1.3	5.0E-02	AJ242625.1	NT	Mus musculus Drmp-1 gene, exons 1-8
7437	20114	33202	12.48	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10100	22748	35963	1.28	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10821	23167		0.45	5.0E-02	BF213260.1	EST_HUMAN	601844753F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E-02	U67600.1	NT	Methanococcus jennaschii section 142 of 150 of the complete genome
11858	25248		3.5	5.0E-02	Q04037	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13158	25800	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13158	25801	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	18043	28692	2.53	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3556	16311		0.69	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632828 3': similar to contains Alu repetitive element: contains element MSR1 repetitive element:
3578	16334	28978	0.99	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3579	16334	28979	0.99	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	17519	30142	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5286	18091	30751	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7042	19733	32783	0.91	4.9E-02	AED00980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AEO02309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8852	21344	34489	0.71	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191	22839	36054	0.48	4.9E-02	P18532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36386	0.46	4.9E-02	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018

Table 4

## Single Exon Probes Expressed in Brain

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11378	23985	37285	3.22	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12345	24752		1.77	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12598	24912		3.41	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
476	13262	25899	9.96	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14997	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3203	15966	28820	2.1	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4823	17358		1.15	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5144	17863	30478	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
5144	17863	30479	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33894	1.32	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0128-221099-012-b02 ST0128 Homo sapiens cDNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
8027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
6731	19565	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	Y287T09.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
6819	19480	32503	2.02	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
8852	21543	34690	0.86	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8875	21566		2.68	4.7E-02	AB026678.1	NT	Gallus gallus Wpict-8 gene, complete cds
9127	21815	34981	6.89	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9547	22200	35392	0.67	4.7E-02	BF308237.1	EST_HUMAN	601892892FT NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4138414 6'
8935	22287		0.57	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10654	23345	36582	1.4	4.7E-02	6764585	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11545	24145	37493	1.39	4.7E-02	U73921.1	NT	Mus musculus paired box protein (pax-6) gene, partial cds
11545	24145	37494	1.39	4.7E-02	U73921.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
264	13072	25712	0.93	4.6E-02	BE163693.1	EST_HUMAN	PM0-HT0339-261199-003-g05 HT0339 Homo sapiens cDNA
722	13498	26149	2.91	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1269	14018		0.89	4.6E-02	A1014265.1	EST_HUMAN	em50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1638979 3' similar to TR:P90533
1338	14080	26762	3.47	4.6E-02	AV727059.1	EST_HUMAN	P80633 LIMA ; contains element LTR1 repetitive element;
							AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'

Page 142 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2492	16208	27951	2.31	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NCJ_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1;
2811	13072	25712	1.9	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
3325	16774	28423	0.74	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251198-003-g06 HT0339 Homo sapiens cDNA
3487	15774	28423	0.73	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
4103	16846		1.35	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase II/Gu (dab21) gene, complete cds
5121	17839	30455	0.89	4.6E-02	AA079157.1	EST_HUMAN	zm92c10.s1 Stratiogene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5847	18442	31366	1.57	4.6E-02	AF076992.1	NT	Haplochromis burtoni gonadotroph-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6136	18914	31883	3.51	4.6E-02	X81624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6136	18914	31884	3.51	4.6E-02	X81624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6702	19617	32659	1.47	4.6E-02	AI149574.1	EST_HUMAN	qc60b06.x1 Soares, placenta, 8to8weeks, 2NHP869W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L.13 L1 repetitive element;
8554	21246	34386	2.69	4.6E-02	BE154008.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11379	23986	37266	4.94	4.6E-02	AA913328.1	EST_HUMAN	cl27h09.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12325	24744		1.88	4.6E-02	AV712871.1	EST_HUMAN	AV712871 DCA Homo sapiens cDNA clone DCAZF07 5'
12705	24885		3.98	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
434	13220	25868	1.72	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1198	13948	26612	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1198	13948	26613	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2103	14834	27568	3.76	4.5E-02	AE003964.1	NT	Xylaria fastidiosa, section 110 of 229 of the complete genome
3710	18463	29102	3.66	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6137	18915	31885	1.61	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6415	19183	32182	0.77	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6779	18523	32550	0.61	4.6E-02	L26487.1	NT	Methanosarcina fissa carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
6779	18523	32551	0.61	4.5E-02	L26487.1	NT	Methanosarcina fissa carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8262	20986	34125	1.96	4.6E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
9849	22499	35689	4.57	4.5E-02	AA325216.1	EST_HUMAN	EST128167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
10000	22648	35680	0.48	4.5E-02	X95508.1	NT	A.europaeum mRNA for legum-like protein

Page 143 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10118	22764	35976	0.85	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12154	24640	31097	1.94	4.5E-02	11418073	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12537	25280	30793	6.91	4.5E-02	AA191097.1	EST_HUMAN	Z443F1.1 Striatum hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	13025		5.52	4.4E-02	BE972733.1	EST_HUMAN	601662154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3936388 5'
2089	14821		5.42	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27953	2.4	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3631	16384	28024	1.85	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4584	17319	29945	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4584	17319	29946	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4693	17427		2.28	4.4E-02	AJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7018	18710	32766	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	18710	32767	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8650	21342	34486	2.14	4.4E-02	AA736669.1	EST_HUMAN	nm13h03.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11007	23679	36936	2.62	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11197	23824	37104	2.78	4.4E-02	AA498739.1	EST_HUMAN	ae33704.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
11890	24460		2.57	4.4E-02	AB040826.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12067	25408		1.87	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
763	13536	26195	7.07	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2573	16287	28024	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3423	16180	28830	7.84	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3651	16404		1.37	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5152	17869	30482	0.95	4.3E-02	U11788.1	NT	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6404	19173	32172	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6633	18395	32410	0.73	4.3E-02	AA652266.1	EST_HUMAN	ns68c12.s1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188886
8411	21104	34243	0.73	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700	21392	34537	1.02	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8700	21392	34538	1.02	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
803	13576	26238	2.7	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
846	13816		2.32	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

Page 144 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
876	13945	26315	1.35	4.2E-02	AW003845.1	EST_HUMAN	w34g01.x1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:2645684 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element;
1714	14457		1.02	4.2E-02	AL445068.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1771	14513	27213	1.01	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3853	16408	29047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	29471	0.7	4.2E-02	BE262605.1	EST_HUMAN	601150933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	29848	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4284	17023	29849	1.83	4.2E-02	U26874.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4855	17429	30060	2.32	4.2E-02	BF342895.1	EST_HUMAN	602017105F1 NCI CGAP_Bm94 Homo sapiens cDNA clone IMAGE:4152672 5'
5530	18328	31231	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5530	18328	31232	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6866	17962	30517	0.56	4.2E-02	BE268285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5'
7426	20103	33190	4.7	4.2E-02	AF278762.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8710	21402	34547	3.96	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10064	22712	35930	1.22	4.2E-02	Q16660	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-66)
10969	23645	36898	2.82	4.2E-02	AA979118.1	EST_HUMAN	6033b11.st NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11278	23939	37231	2.64	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11278	23939	37232	2.64	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11469	24090	37402	1.68	4.2E-02	AF179458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12415	25335		3.43	4.2E-02	A193494.1	EST_HUMAN	w48g10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
497	13281	25916	1.24	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2683	15392	28131	1.04	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4438	17175		7.52	4.1E-02	AW883484.1	EST_HUMAN	QV1-NN0012-180400-184-006 NN0012 Homo sapiens cDNA
5556	18353	31262	0.82	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5556	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6783	18527		0.67	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
6959	19691	32742	1.25	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7413	20090	33174	2.09	4.1E-02	7662347	NT	Homo sapiens KIAA0887 protein (KIAA0887), mRNA

Page 145 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7602	20173	33285	0.66	4.1E-02	L02110.1	NT	Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8541	21233	34376	0.68	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9062	21741	34899	0.81	4.1E-02	AJ372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25336	30715	4.07	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3238	16000	28690	3.28	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5295	18100	30769	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18898	31866	0.93	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3588380 3' similar to TR:076286 O76286 R29124.1;
7660	20258	33386	6.57	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7668	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7668	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	21308	34451	2.22	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1 4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	BF679378.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9567	22220	35406	4.01	4.0E-02	AJ000941.1	NT	Melhanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
9884	22634		1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24369		1.54	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cat+ ATPase
12063	26158	30898	3.31	4.0E-02	AJ001086.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1088	13856	26516	2.75	3.9E-02	BF516149.1	EST_HUMAN	UIH-BW1-arr-h-08-Q-UJ1st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1654	14889	27402	2.4	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2708	16415		1.69	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118	16860	29487	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16860	29488	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

Page 146 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5644	18439	31353	1.04	3.9E-02	BE068841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5766	18557	31484	0.95	3.9E-02	BF075203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
6957	19439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435	33557	1.14	3.9E-02	BF236613.1	EST_HUMAN	601806848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134778 5'
7959	20654	33778	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20654	33779	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11386	20398	33511	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25298		15.38	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24883		1.83	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12668	26223		5.31	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, nmxa28orf
1945	14680	27394	1.16	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.8E-02	AJ251973.1	NT	Homo sapiens partial steatrin-1 gene
4876	17603	30228	1.1	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM/2001698 5'
5354	18157	30840	1	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
5998	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7218	19603	32976	1.66	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8582	21254		1.33	3.8E-02	M00675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10548	23245	36481	2.62	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
971	13736	28401	4.94	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1367	14115	28780	0.91	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2280	14958	27998	3.84	3.7E-02	AJ984806.1	EST_HUMAN	wf85a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2532	15298	28034	0.92	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	18811	28457	0.9	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3047	15813	28458	2.99	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203		1.17	3.7E-02	6880541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnnm3), mRNA
6978	26422		0.83	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7

Page 147 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7592	20260	33368	0.56	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
9914	22563		1	3.7E-02	AA782516.1	EST_HUMAN	al55c09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone 1360912 3'
11954	24506	37811	3.86	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12603	25193	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3648	16369	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3654	16407	29046	0.89	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5341	18144	30808	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30921	0.64	3.6E-02	AF181722.1	NT	Homo sapiens RIZAS (RU2) mRNA, complete cds
6007	19370	32382	5.47	3.6E-02	AW945518.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6607	19370	32383	5.47	3.6E-02	AW945518.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6986	19678	32726	2.5	3.6E-02	AF026952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
7208	19891	32967	2.76	3.6E-02	AA714521.1	EST_HUMAN	rw20a06.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7533	20203	33298	1.03	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN)
8291	21958	35130	1.72	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-508 HT0158 Homo sapiens cDNA
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22165	35347	0.83	3.6E-02	BF347586.1	EST_HUMAN	602020453F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156116 5'
11136	23903	37080	1.4	3.6E-02	BF131608.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11139	23903	37081	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11852	24436		1.46	3.6E-02	AI280966.1	EST_HUMAN	ql48509.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1872185 3'
876	13644	26314	1.08	3.6E-02	U08508.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
988	13751	26413	1.39	3.6E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1556	14303	26891	1.55	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1558	14303	26982	1.55	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4188	16329	29559	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4281	17020	29847	1.27	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6127	18905	31873	1.77	3.5E-02	J01238.1	NT	Malze actin 1 gene (MAc1), complete cds

Page 148 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20372		0.78	3.5E-02	H28951.1	EST_HUMAN	jp44a05.1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:180256 5' similar to contains Alu repetitive element;
8521	21213	34357	2.7	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
9917	22566	35752	1.45	3.5E-02	X76642.1	NT	Llactis MG1363 grpE and dnaK genes
9955	22813	35817	0.5	3.5E-02	BE561042.1	EST_HUMAN	601344801F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877654 5'
11477	24078	37388	1.82	3.5E-02	AW681641.1	EST_HUMAN	PM1-C10326-291289-002-R03 C10326 Homo sapiens cDNA
11477	24078	37389	1.82	3.5E-02	AW681641.1	EST_HUMAN	PM1-C10326-291289-002-R03 C10326 Homo sapiens cDNA
12598	25234		5.89	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13789	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	xx26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1184	13836		7.14	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2391	15112	27849	2.06	3.4E-02	T57160.1	EST_HUMAN	ys20e08.11 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3424	16181	28831	1.4	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	16509	28145	0.7	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
3900	16850	29291	3.19	3.4E-02	AW794952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4559	17284	29922	2.41	3.4E-02	X59799.1	NT	Mmusculus S-anigen gene promoter region
5000	17723		3.59	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5019	17740	30349	1.2	3.4E-02	AJ012489.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6764	17923	30558	4.73	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8159	20853		3.25	3.4E-02	AI889629.1	EST_HUMAN	w199d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
8946	21338	34482	1.36	3.4E-02	AA694886.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1218071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:928749 3' similar to TR:G1017425 G1017425 ;
8814	21506		5.97	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTL SRGVPLKATMRNTEITAE LTNLKESVTADAGRYEITANSSGTTKAFINNVLD RPPG
9578	22330		0.63	3.4E-02	AI092719.1	EST_HUMAN	PPT GPVAVISDITEESVTLKWEPPKYDGGSVTYNLLKRETS TAVWTEVSATVARTMVKMKL ... ;
963	13161		9.61	3.3E-02	AB398735.1	EST_HUMAN	ox99h08.x1 Soares_papillary_thyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1683619 3'
1143	13898	26559	17.86	3.3E-02	AB038867.1	NT	z175e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
							Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds

Page 149 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14238	26923	1.16	3.3E-02	L16870.1	NT	Homo sapiens cytochrome P450C18 (CYP2C18) gene, exons 2 and 3
1635	14381	27068	1.47	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2077	14609		2.46	3.3E-02	R00112.1	EST_HUMAN	Y25c09.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27910	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Ttr1), mRNA
4156	14381	27068	2.44	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4435	17171	29800	1.78	3.3E-02	6765962	NT	Mus musculus tumor rejection antigen gp98 (Ttr1), mRNA
6336	19108	32095	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19108	32096	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20085	33169	0.63	3.3E-02	AF124182.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (cns5) gene, partial cds
9222	21901	35071	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21901	35072	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35162	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9324	21991	35163	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11065	23735	37008	3.63	3.3E-02	BF691107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
12142	24630		3.24	3.3E-02	T96545.1	EST_HUMAN	602247171F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:4332497 6'
12259	24704		1.52	3.3E-02	AF289665.1	NT	ye49f11.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121101 5'
12288	24718		2.92	3.3E-02	M81890.1	NT	Mus musculus EIF-4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
129	12944	25938	0.74	3.2E-02	AJ002005.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
1104	13861	26520	7.01	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1104	13861	26521	7.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1104	13861	26521	7.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2112	14843		3.01	3.2E-02	P28995	SWISSPROT	LARGE TEGUMENT PROTEIN
3131	15898	28540	10.08	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3846727 6'
3701	16454	28094	0.92	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3942	16692	29330	1.84	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3942	16692	29331	1.84	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4183	16634		14.21	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4894	17621		1.09	3.2E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, GBA, NG22, G9, HSP70, HSP70, HSC70, and antRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5448	18247	31135	1.83	3.2E-02	X68709.1	NT	S.griseocapneum whiG-Stv gene

Page 150 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18247	31136	1.83	3.2E-02	X68709.1	NT	S. griseocarnum whlG-Stv gene
6431	19189	32198	3.13	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6432	19200		33.46	3.2E-02	T89387.1	EST_HUMAN	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element ;
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Saguius oedipus tissue kallikrein gene, complete cds
7682	20326	33436	0.64	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8189	20893	34030	4.64	3.2E-02	6880565	NT	Mus musculus kinesin family member 3c (KIF3c), mRNA
8839	21531		0.73	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8126	21813	34978	1.21	3.2E-02	A1276971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9126	21813	34979	1.21	3.2E-02	A1276971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9957	22605		4.07	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10266	22804	36114	0.95	3.2E-02	U98782.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	13986		2.14	3.1E-02	4803416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1282	14032	26702	1.72	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14622	27332	1.09	3.1E-02	6871564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1867	14703		1.34	3.1E-02	Z60097.1	NT	Drosophila melanogaster mRNA for headcase protein
5182	17990	30506	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5276	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:703858 5'
5581	18356	31268	0.74	3.1E-02	BF887742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066789 5'
5628	25072	31338	0.59	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (fhaB- and fhaC-homologs, unknown genes) and flanking genes, strain FAM18
8840	21532	34677	0.46	3.1E-02	BE665092.2	EST_HUMAN	601658876R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
8831	22579	35778	2.83	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
11765	24356	37689	1.78	3.1E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
1619	14366		1.88	3.0E-02	AF187125.1	NT	Plykethines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2500	15304	28040	0.97	3.0E-02	AA402242.1	EST_HUMAN	z665103.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3846	16398	28038	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	16480		0.74	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e08 ST0298 Homo sapiens cDNA
3826	16679		1.42	3.0E-02	AA364003.1	EST_HUMAN	ESTT4530 Pineal gland II Homo sapiens cDNA 5' end
4991	17714	30318	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds

Page 151 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6160	18937	31905	1.4	3.0E-02	N89815.1	EST_HUMAN	z339a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284908 5' similar to contains element TAR1 repetitive element;
6160	18937	31906	1.4	3.0E-02	N89815.1	EST_HUMAN	z339a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284908 5' similar to contains element TAR1 repetitive element;
6892	18609	32848	3.32	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6806	19467	32488	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6806	19467	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6871	19463	32472	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6871	19463	32473	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19819	32885	1.4	3.0E-02	MB6524.1	NT	Human dystrophin gene
7483	20155		0.59	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154394F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285654 5'
8839	21231	34373	0.66	3.0E-02	BF338899.1	EST_HUMAN	IL5-HT0704-280500-108-c04 HT0704 Homo sapiens cDNA
8892	21384		1.8	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	23004	36221	1.49	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 138 of the complete genome
10448	23092	36322	0.49	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23862	37148	2.73	3.0E-02	MB1357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ns87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12243	25389	30618	2	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12587	24809		2.46	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12629	25383		2.06	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosyltransferase beta-1,4-galactosyltransferase mRNA, complete cds
2436	15594	27891	1.27	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2890	15758	28402	1.04	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3880695 5'
2890	15758	28403	1.04	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3880695 5'
3308	16658	28289	0.89	2.9E-02	HT2805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18754	31715	0.87	2.9E-02	AF000221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6189	18975	31953	7.39	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855598 5'
6855	19555	32585	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32904	12.03	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

Page 152 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	20592	33723	0.87	2.9E-02	AF128278.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20592	33724	0.87	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
8558	22211	35396	2.49	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
8558	22211	35397	2.49	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9774	22425		0.75	2.9E-02	AW976697.1	EST_HUMAN	EST388706 MAGe resequences, MAGN Homo sapiens cDNA
10243	22891	38103	1.25	2.9E-02	AF000094.1	NT	Aeropyrum pernix genomic DNA, section 777
10977	17602	30590	1.91	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
562	13335		0.96	2.8E-02	AW970163.1	EST_HUMAN	EST382234 MAGe resequences, MAGK Homo sapiens cDNA
3360	18119	28775	1.3	2.8E-02	AF066083.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3360	18119	28776	1.3	2.8E-02	AF066083.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5400	18200	30905	11.82	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6711	19626	32670	1.15	2.8E-02	T78960.1	EST_HUMAN	y421b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108865 5'
8228	20820	34058	1.81	2.8E-02	AJ005820.1	NT	Craterostigma planlagneum mRNA for homeodomain leucine zipper protein (hb-1)
8915	21608	34749	0.85	2.8E-02	AA280762.1	EST_HUMAN	z696c06.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9708	21796	34960	1	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9212	21891	35058	0.89	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R06968.1	EST_HUMAN	y12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128675 5'
12630	24876		1.48	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S9A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
1472	14219	26905	1.23	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3425	16182	28832	1.74	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4178	16918	20645	1.92	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:280487 5'
4178	16918	29548	1.92	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:280487 5'
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	y93k09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128667 5' similar to SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS :
5312	18601	31529	0.86	2.7E-02	X61870.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
5885	18671	31612	0.64	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6305	19270		0.93	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
6367	19449	32467	2.29	2.7E-02	AA993571.1	EST_HUMAN	cd96h03.s1 Soares_total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:1824661 3'

Page 153 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8252	20946		1.08	2.7E-02	AI377036.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8514	21206	34349	0.49	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
658	13340	26668	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2389	18088	27825	3.29	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 887202 Homo sapiens cDNA clone IMAGE:839595 3'
2368	15090	27827	4.48	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2368	15090	27828	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2916	15682		1.86	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G8A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4847	17577	30200	2.25	2.6E-02	L12032.1	NT	Chicken dorsoalis-1 mRNA, complete cds
5005	17728	30332	1.56	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5032	17762	30384	2.35	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5764	18546		0.7	2.6E-02	AL161563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5800	18590		0.59	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6125	18903		7.34	2.6E-02	A1206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6331	19101	32089	1.9	2.6E-02	BE621748.1	EST_HUMAN	gg27111.x1 NCI CGAP_Ki68 Homo sapiens cDNA clone IMAGE:1762317 3'
6728	19562	32583	0.9	2.6E-02	Z99004.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6728	19562	32594	0.9	2.6E-02	Z99004.1	NT	Vaccinia virus ORF1L, strain Wyeth
6810	19471	32494	7.11	2.6E-02	6881271	NT	Vaccinia virus ORF1L, strain Wyeth
8403	21098	34232	0.71	2.6E-02	AA850346.1	EST_HUMAN	Rattus norvegicus Nerve growth factor receptor, fast (Ngf), mRNA
9260	22014	35182	1.15	2.6E-02	11432020	NT	ak22f04.st Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
9814	22287	35463	0.75	2.6E-02	AF114952.1	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9814	22287	35464	0.75	2.6E-02	AF114952.1	NT	Saccharomyces diereensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10303	22850	36165	4.39	2.6E-02	AL163303.2	NT	Saccharomyces diereensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11197	23856		1.67	2.6E-02	4508468	NT	Homo sapiens chromosome 21 segment HS21C103
11361	24049		2.33	2.6E-02	AA278351.1	EST_HUMAN	Homo sapiens radixin (RDX) mRNA
11553	24162	37465	2.2	2.6E-02	AW500547.1	EST_HUMAN	zs84c02.r1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:704162 5'
12170	26375	30615	2.09	2.6E-02	BF343827.1	EST_HUMAN	UI-HF-BNO-aki-s-10-U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077468 5'
519	13303	25935	1.75	2.6E-02	AI793130.1	EST_HUMAN	602015501F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4180944 5'
519	13303	25936	1.75	2.6E-02	AI793130.1	EST_HUMAN	on28f06.y6 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
781	13563	26224	15.9	2.6E-02	BE974314.1	EST_HUMAN	on28f06.y6 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
							601680309R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950965 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
849	13619	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950666 3'
2768	15471		2.24	2.5E-02	U12571.1	NT	Rattus norvegicus ribophyllin-3A mRNA, complete cds
2956	15722	28371	4.35	2.5E-02	X99897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2968	15722	28372	4.35	2.5E-02	X99897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17879	29399	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4023	17879	29400	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4182	16922	29550	4.23	2.5E-02	AW592114.1	EST_HUMAN	H36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934016 3'
5625	18422	31335	0.61	2.5E-02	AI732776.1	EST_HUMAN	z63c10.x5 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:810364 3'
6100	18878		5.01	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element
6115	18893		4.1	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6244	19018	31992	1.04	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33336	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
7563	20233	33337	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34850	0.81	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8863	21554	34698	0.47	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2516370 3'
9968	22614		0.55	2.5E-02	X71303.1	NT	D. rerio 28S ribosomal RNA, D2 domain
10482	23128	36356	0.65	2.5E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3'
10712	23401	36840	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10712	23401	36841	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10773	23456	36700	2.32	2.5E-02	A1237636.1	NT	Bos taurus partial stat5B gene, exons 17-19
10785	23478						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ii alpha) and major histocompatibility protein class II beta chain (Ii beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II>
11770	24361		3.46	2.5E-02	AF090157.1	NT	Homo sapiens gene for LECT2, complete cds
12134	25311		2.55	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
12311	25182		2.89	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12432	24804	31043	1.94	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1593	14339	27028	1.7	2.4E-02	H65984.1	EST_HUMAN	y75f1.1.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:211149 5'
2037	15584	27501	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27502	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4335	17074	29702	1.65	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4485	17220	29847	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	17220	29848	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

Page 155 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6068	17787	30403	0.95	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6121	18899	31897	0.9	2.4E-02	W86680.1	EST_HUMAN	z163h04.s1 Soares fetal liver spleen 1NfLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6267	18040	32016	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6287	18040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	18809	32875	0.8	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7138	18825	32892	0.8	2.4E-02	X12825.1	NT	Rat gene for uncoupling protein (UCP)
7138	18825	32893	0.9	2.4E-02	X12825.1	NT	Rat gene for uncoupling protein (UCP)
7791	20488		0.72	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
7844	20539		0.5	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8340	21033		0.69	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:233678 3' similar to contains Alu repetitive element; contains A3R repetitive element
8428	21122	34260	8.78	2.4E-02	N69442.1	EST_HUMAN	z335g11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:284588 3' similar to gb K02809 RA.TSR7K Rat (RNA); contains A3R.b1 A3R repetitive element
8885	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8907	21698	34740	0.78	2.4E-02	AA625680.1	EST_HUMAN	z335g11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element
8991	22244	35427	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphuryase (cnx5) gene, complete cds
9591	22244	35428	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphuryase (cnx5) gene, complete cds
9708	22357	35553	2.38	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GK Homo sapiens cDNA clone GKCDSC03 5'
9881	22531	35728	2.73	2.4E-02	AA493894.1	EST_HUMAN	nh07b12.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
10512	23158		0.46	2.4E-02	BE387111.1	EST_HUMAN	60127492F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615802 5'
11565	24164	37475	1.89	2.4E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11565	24164	37476	1.89	2.4E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11938	24495		2.28	2.4E-02	9827809	NT	Bacteriophage b11.87, complete genome
12081	24589	31124	1.81	2.4E-02	6753635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
12136	24625	31094	2.37	2.4E-02	BE928869.1	EST_HUMAN	MR0-F10175-310800-202-a08 F10175 Homo sapiens cDNA
12186	24657	31063	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

Page 156 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12186	24657	31104	1.68	2.4E-02	U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12216	24878		1.34	2.4E-02	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12360	24784		3.88	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1885	14603		4.28	2.3E-02	W05340.1	EST_HUMAN	zab4g08.t1 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:289284 5'
1890	14617		10.45	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2350	15072	27809	2.08	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3670	16423	29084	6.18	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3702	16455		0.8	2.3E-02	L23429.1	NT	Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3' end
4129	16871	29489	1.06	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4129	16871	29500	1.08	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	29755	0.93	2.3E-02	AW869107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4415	17152	29780	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4416	17880	29782	1.14	2.3E-02	AW693693.1	EST_HUMAN	xs25d08.x1 NCJ CGAP U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4416	17880	29783	1.14	2.3E-02	AW693693.1	EST_HUMAN	xs25d08.x1 NCJ CGAP U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4555	17290	29919	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4555	17290	29920	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5291	18096	30759	3.63	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6522	19288	32292	4.08	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6893	17959	30513	0.69	2.3E-02	BE141476.1	EST_HUMAN	MIR0-H10080-011069-002-c09 H10080 Homo sapiens cDNA
7776	20472	33595	6.28	2.3E-02	U63610.1	NT	Human plecln (PLEC1) gene, exons 3-32, and complete cds
8370	21093	34204	0.94	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8370	21093	34205	0.94	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34429	0.68	2.3E-02	A1685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8597	21289	34430	0.68	2.3E-02	A1685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9036	21726	34880	0.98	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9759	22410	35617	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9929	22577	35776	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9929	22577	35777	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Bacillus licheniformis isolate N57N1 KerA gene, partial cds

Page 157 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10682	23373	36916	2.16	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12058	28168		5.07	2.3E-02	BE278331.1	EST_HUMAN	601179558F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12562	24892	30997	2.16	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12618	25409		2.42	2.3E-02	U11077.1	NT	Dictyostellium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12807	25260		1.62	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
720	13494	26147	4.13	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1741	14483		1.38	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
3428	16185		1.49	2.2E-02	AA577765.1	EST_HUMAN	nm24a04.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3637	18390		4.01	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3834	16585	29221	1.26	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3899	16549	29280	0.75	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5008	17729	30333	1.05	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7146	19833	32902	3.63	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8269	20863	34104	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8269	20963	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X79468.1	NT	P.vulgata alpha tub 2 mRNA
9586	22239	35422	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9586	22239	35423	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10105	22753		0.89	2.2E-02	8678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11167	23834	37115	1.66	2.2E-02	BE797601.1	EST_HUMAN	6011584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
11841	24425	37766	1.54	2.2E-02	11423632	NT	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
12315	24737		4.07	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
410	13195		6.11	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
436	13222		9.98	2.1E-02	AF029726.1	NT	Dictyostellium discoideum histidine kinase C (dhkC) mRNA, complete cds

Page 158 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	13989	26958	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1366	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1368	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27482	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2028	14763	27483	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2591	16305	28041	1.32	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008920
2819	13534	26193	4.48	2.1E-02	N28266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:284541 5'
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3571	16326	28973	1	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786121 5'
4110	18853	29480	0.81	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	28841	0.81	2.1E-02	BF343655.1	EST_HUMAN	802016306F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4410	17147	29775	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4421	17167	29788	1.53	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4461	17197		0.69	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4662	17396	30031	4.51	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4769	17501	30124	0.76	2.1E-02	A1823432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384628 3'
5553	18350	31259	1.13	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111189-040-h05 HT0244 Homo sapiens cDNA
6968	19448	32468	0.88	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8417	21110	34249	0.6	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9403	22065	35236	0.5	2.1E-02	AA984288.1	EST_HUMAN	am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
9531	22184	35368	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9531	22184	35369	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9883	22533	35730	1.15	2.1E-02	L28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
9981	22609	35814	0.89	2.1E-02	AA984288.1	EST_HUMAN	am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
10622	23168	38395	0.45	2.1E-02	AP001519.1	NT	Bacillus halodurans genomic DNA, section 13/14

Page 159 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11479	24080	37381	1.38	2.1E-02	6764265	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp40a), mRNA
12298	17197		8.02	2.1E-02	Y19213.1	NT	Homo sapiens putative psIHbA pseudogene for hair keratin, exons 2 to 7
12339	23163	30901	1.89	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30989	5.71	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
16	12844	25457	1.1	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MER1.13
17	12845	25458	14.4	2.0E-02	AW895595.1	EST_HUMAN	MER1 repetitive element ;
252	13061	25699	3.76	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
288	13094	25736	2.72	2.0E-02	AA486838.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
781	13553	28214	2.11	2.0E-02	6753635	NT	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:313307 5'
1065	13823	26483	1.6	2.0E-02	AL086805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1177	13930	26595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1177	13930	26598	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1865	14604	27313	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1866	14604	27314	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15508		3.24	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3077	12844	26457	2.11	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MER1.13
3141	15905		1.4	2.0E-02	7305474	NT	MER1 repetitive element ;
3221	15984		2.35	2.0E-02	AF095588.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3988	19736	29370	1.3	2.0E-02	M18085.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5548	18345	31254	0.58	2.0E-02	U34778.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5807	18598	31523	0.7	2.0E-02	L35321.2	NT	Caenorhabditis elegans smn-2 mRNA, complete cds
7460	20126	33217	1.11	2.0E-02	AP000004.1	NT	Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds
7450	20126	33218	1.11	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
9777	22428		2.21	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
10259	22907	36117	1.62	2.0E-02	AI640342.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
10539	23236	36469	1.78	2.0E-02	Z73956.1	NT	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93/162
11682	24277	37598	2.21	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17 20-lyase, complete cds
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA

Page 160 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11880	17809	30595	1.9	2.0E-02	AA48638.1	EST_HUMAN	aa15b10.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12338	15506		1.92	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	28038		6.4	2.0E-02	T80037.1	EST_HUMAN	yj04c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
677	13452	26095	2.15	1.9E-02	AA572764.1	EST_HUMAN	nf18a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1 t1 L1
1611	14358	27047	1.15	1.9E-02	P18488	SWISSPROT	repetitive element
2032	14787	27496	2.68	1.9E-02	AL163303.2	NT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27497	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27968	0.97	1.9E-02	AL161550.2	NT	Homo sapiens chromosome 21 segment HS21C103
2808	16872	28320	7.48	1.9E-02	AA713856.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2952	16718	28369	1.66	1.9E-02	AV648669.1	EST_HUMAN	mw0405.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238387 3'
3598	18351		1.18	1.9E-02	NS2250.1	EST_HUMAN	AV648669 GLG Homo sapiens cDNA clone GLCBLH07 3'
3691	18444		9.58	1.9E-02	BE738088.1	EST_HUMAN	yj28b02.s1 Soares multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:284331 3'
3703	18456	28085	0.95	1.9E-02	AI301183.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839664 6'
4025	18770	29402	1.49	1.9E-02	AF141940.1	NT	gn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element
4170	18910	29539	1.83	1.9E-02	P09081	SWISSPROT	Myoplasma imitans VihA1 precursor (VihA1) and VihA2 precursor (VihA2) genes, partial cds
4170	18910	29540	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	28872	3.21	1.9E-02	AI452999.1	EST_HUMAN	HOMEOTIC BICOID PROTEIN (PRD-4)
4951	15227	27968	4.09	1.9E-02	AL161550.2	NT	j46d04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element
5233	18039	30667	0.99	1.9E-02	AF037352.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5382	18182	30872	1.41	1.9E-02	L47572.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
6701	18495		0.86	1.9E-02	AB018507.1	NT	Maleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
7001	18893	32744	1.38	1.9E-02	U19241.1	NT	Drosophila melanogaster gene for glyceral-3-phosphate dehydrogenase, complete cds
7001	18893	32745	1.38	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469	21161		1.23	1.9E-02	AL162754.2	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9230	21809	35082	1.03	1.9E-02	BF316129.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9613	22266	35452	0.6	1.9E-02	L10114.1	NT	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'
9946	22593	35798	1.05	1.9E-02	BF695832.1	EST_HUMAN	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10152	22800	36017	0.54	1.9E-02	D64001.1	NT	601852385F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4078253 5'
10681	23372	36614	1.44	1.9E-02	AF008938.1	NT	Synochocystis sp. PCC6803 complete genome, 2027, 2539000-2644794
12090	25171	30903	2.82	1.9E-02	AF101055.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12648	25147		1.36	1.9E-02	L11088.1	NT	Hirudo medicinalis intermediate filament glierin mRNA, complete cds
							Candida albicans lambda Ca3/B fragment

Page 161 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
336	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	hns208.x1 NCI_CGAP_C017 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
670	13448	26086	0.93	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1137	13892	26853	1.32	1.8E-02	X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1416	14164	26947	1.73	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encare (enc) mRNA, complete cds
2685	15394	28133	1.71	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 529 of the complete genome
3205	16968		0.94	1.8E-02	AI805929.1	EST_HUMAN	tes2a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
4085	16810		0.99	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408635 3'
4366	17133	29764	1.17	1.8E-02	AW836363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
6712	19627	32671	5.02	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FXW 5'REGION
8029	20724	33857	0.89	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8367	21060	34200	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-169-h08 NN1073 Homo sapiens cDNA
8410	21103	34242	0.8	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9392	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9392	22054	35226	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9542	22195		2.41	1.8E-02	AA897543.1	EST_HUMAN	q16209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbL11672 ZINC FINGER PROTEIN 91 (HUMAN);
9983	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5'
10126	22774	35987	1.37	1.8E-02	X96933.1	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11613	24211	37535	1.59	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (617)
11628	24223	37545	3.32	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
886	13653	26323	1.86	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1783	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1783	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1864	14602		3.41	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2108	14837		10.5	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2291	15016	27752	0.99	1.7E-02	S74186.1	NT	[microsatellite INRA41] Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2646	16366		1.01	1.7E-02	7657485	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2898	15762	28411	1.44	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'

Page 162 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3502	16256		4.67	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3614	16367		0.73	1.7E-02	P04929	SWISSPROT	MER19.b1 MER19 repetitive element ; HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	AA669818.1	EST_HUMAN	ec18f04.s1 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu
4176	16916		2.04	1.7E-02	R02506.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element ; ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4420	17166	29787	1.49	1.7E-02	A1305279.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb.X52359 ZINC
4491	17227	29856	1.78	1.7E-02	AW673183.1	EST_HUMAN	FINGER PROTEIN 30 (HUMAN); hm34a03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains
4666	17400	30034	1.61	1.7E-02	V00641.1	NT	L1.1 L1 repetitive element ; Messenger RNA for anglerfish ( <i>Lophius americanus</i> ) somatostatin II
4763	17495		5.84	1.7E-02	A1015076.1	EST_HUMAN	ov51e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
5007	17730	30334	0.69	1.7E-02	6881289	NT	Rattus norvegicus N-arginine diase convertase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 wg35f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to
8035	18815	31775	2.07	1.7E-02	A1769247.1	EST_HUMAN	contains Alu repetitive element;
8494	19261	32250	1.47	1.7E-02	A1038280.1	EST_HUMAN	oy85f03.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
6950	19432	32448	1.27	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19791	32856	2.44	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7267	19941	33016	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7267	19941	33017	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7842	20307		1.78	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9336	20407	33523	0.98	1.7E-02	U21854.1	EST_HUMAN	Caenorhabditis elegans cCAF1 protein gene, complete cds
9598	22251	35437	1.3	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434f0314.1_1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434f0314 5'
11801	24391	37724	1.38	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MISE55), mRNA
12631	25337	30716	2.39	1.7E-02	AW903482.1	EST_HUMAN	GM4-NN1030-040400-130406 NN1030 Homo sapiens cDNA
498	13282		3.19	1.8E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1653	14398	27088	1.04	1.8E-02	Y18899.1	NT	Treponema maltophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2246	14974	27711	0.9	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.9	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15294	28022	1.05	1.8E-02	AJ006345.1	NT	Homo sapiens KVLQY1 gene
2649	15359	28102	1.48	1.8E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2699	15408		0.96	1.8E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds

Page 163 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3018	15782	28431	0.71	1.6E-02	AF112282.1	NT	Lasaea sp. isolate IBD cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28028	5.9	1.6E-02	AW850652.1	EST_HUMAN	IL3-C10219-160200-063-C07 C10219 Homo sapiens cDNA
3830	16581	29215	1.32	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4154	16896		2.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fes-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4267	17007	29840	0.97	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-407 PT0012 Homo sapiens cDNA
5536	18334	31241	1.25	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6548	19311	32316	2.05	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6832	19494	32517	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	0.86	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33847	0.76	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8078	20772		1.88	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
8940	22588		2.72	1.6E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22866	36184	1.29	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P28294 TELOKIN, [1]:
10319	22866	36185	1.29	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P28294 TELOKIN, [1]:
10828	26132	36748	2.38	1.6E-02	Z94828.1	NT	G. gallus microsatellite DNA (LE0260 (=T16IIIET1))
11174	23841	37124	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11174	23841	37125	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11495	24098	37407	1.54	1.6E-02	AJ373558.1	EST_HUMAN	q286a10.x1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
734	13508		23.05	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2138	14888	27598	4.24	1.5E-02	N39521.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2172	14901	27635	1.69	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3057	15823	28467	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3057	15823	28468	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3711	16464	29103	0.98	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-512 TN0115 Homo sapiens cDNA
6201	18977	31955	1.56	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7219	19904		1.63	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7301	19984	33060	1.2	1.6E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA

Page 164 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20469	33592	1.63	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20476	33602	3.59	1.5E-02	11417739	NT	Homo sapiens vely-IRNA synthetase 2 (VAR52), mRNA
8729	21421	34565	0.9	1.5E-02	BF345554.1	EST_HUMAN	602019135f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5'
9368	21943		0.51	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22079	35251	1.47	1.5E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9711	22362	35559	0.98	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.98	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23780	37068	3.49	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11163	23830	37109	2.14	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11858	24440	37781	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	25214		1.74	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12787	25039		1.46	1.5E-02	A1763127.1	EST_HUMAN	wf06h03.x1 NCI_CGAP_Q11 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element;
408	13193		2.29	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AF39, section 58 of 94 of the complete genome
1098	13854	26613	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13983		1.24	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1375	14123		1.45	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1607	14253		1.25	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAH11 5'
3207	15970	28622	2	1.4E-02	AF160969.2	NT	Bifidobacterium longum Ne+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine-xylose repressor protein (nagCxyR) gene, partial cds
3393	16152	28605	1.07	1.4E-02	AW074212.1	EST_HUMAN	x609d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3478	16234	28888	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28889	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3648	16401	29041	6.63	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29817	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGG Homo sapiens cDNA
4455	17191	29818	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGG Homo sapiens cDNA
4821	17552	30174	7.21	1.4E-02	BE733142.1	EST_HUMAN	601667403f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601667403f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	19091	32079	5.47	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;

Page 165 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	18091	32080	5.47	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Bi2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8786	21488	34634	0.75	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9053	21742	34900	0.84	1.4E-02	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21987	35141	2.27	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11985	24526	37287	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12601	24913		2.36	1.4E-02	11428968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27395	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 6'
3208	15971	28624	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
4874	17601	30223	0.93	1.3E-02	U68061.1	NT	Human germine T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
5166	17875	30532	1.31	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5166	17975	30533	1.31	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
6072	18851	31818	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6105	18883	31851	0.88	1.3E-02	M62962.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6865	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6865	17942	30536	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7477	20150	33244	4.9	1.3E-02	AI031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8380	21073	34212	1.65	1.3E-02	AF156891.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107	22755	35967	1.81	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22826	36040	0.68	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10913	23593	36838	3.97	1.3E-02	AW268563.1	EST_HUMAN	xc44e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36839	3.97	1.3E-02	AW268563.1	EST_HUMAN	xc44e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

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12337	25352		1.44	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12437	24807		2.41	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12807	25145		28.18	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	25783	3.48	1.2E-02	AA059299.1	EST_HUMAN	z65601.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element
440	13228	25869	1.66	1.2E-02	P38898	SWISSPROT	L1 repetitive element
721	13495	26148	2.02	1.2E-02	A183522.1	EST_HUMAN	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
2176	14904	27637	1.81	1.2E-02	AL163213.2	EST_HUMAN	q68e12.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1794670 3' similar to contains L1.11 L1
2178	14907	27640	1.71	1.2E-02	AV731704.1	NT	repetitive element
2444	15163	27801	1.39	1.2E-02	AW172350.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2642	16163	27901	1.07	1.2E-02	AW172350.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
3058	15963		6.68	1.2E-02	AA075418.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3281	16042	28691	2.1	1.2E-02	R62805.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3284	16045	28694	0.92	1.2E-02	A1669894.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:645020 5'
4675	17409	30045	0.91	1.2E-02	A1887378.1	EST_HUMAN	x11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
							z68e07.x5 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains
							element MER22 repetitive element
							wm39f0.4.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2498336 3'
4659	17588	30211	2.03	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis
4981	17704		1.13	1.2E-02	AB019786.1	NT	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP79) gene, complete cds
6025	17748	30358	1.41	1.2E-02	AV731704.1	EST_HUMAN	Cynops pirhogaster CpUbiq1 mRNA, partial cds
5666	18461	31375	1.73	1.2E-02	D76589.1	NT	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
6026	18806	31767	0.72	1.2E-02	AF045555.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6907	18845	32691	6.46	1.2E-02	AF175412.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and
7192	19878	32952	1.36	1.2E-02	H02197.1	EST_HUMAN	replication factor C subunit 2 (RFC2) gene, complete cds
7212	19897	32972	10.54	1.2E-02	AV732093.1	EST_HUMAN	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7456	20130	33222	0.57	1.2E-02	BF216650.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150696 3'
							AV732093 HTF Homo sapiens cDNA clone HTFBIC09 6'
							601882849F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
7896	20591	33722	2.18	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-
8092	20786	33917	1.35	1.2E-02	AF183612.1	NT	GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-
8092	20786	33918	1.35	1.2E-02	AF183612.1	NT	GALNAAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
							Homo sapiens fringe protein mRNA, partial cds
							Homo sapiens fringe protein mRNA, partial cds

Page 167 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8788	21480		1.03	1.2E-02	T76987.1	EST_HUMAN	yt72c08.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35378	2.48	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9570	22223	35408	1.35	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUJ) (HPER)
12619	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujilwara) Homo sapiens cDNA clone GEN-557G06 5'
1246	13985	26662	1.49	1.1E-02	AA070364.1	EST_HUMAN	zm69a1.1.s1 Striatogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1701	14444	27143	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2031	14766	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2880	16647		4.05	1.1E-02	N99623.1	EST_HUMAN	za40a05.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296040 5'
3513	16269	28924	2.98	1.1E-02	AI553508.1	EST_HUMAN	tg95b10.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPFF_HUMAN
4086	16829		0.86	1.1E-02	AW813786.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30132	1.5	1.1E-02	AL046383.2	EST_HUMAN	DKFZp568E0924 s1 598 (synonym: hute1) Homo sapiens cDNA clone DKFZp568E0924
6057	18837	31789	1	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spovK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (ghsA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl
7497	20169	33281	2.51	1.1E-02	BE149611.1	EST_HUMAN	RC1-HIT0258-100300-016-h07 HT0258 Homo sapiens cDNA
8538	21230	34372	0.91	1.1E-02	AW995160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8721	21413	34556	0.87	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
8800	21492	34639	6.45	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9829	22480	35682	2.03	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Striatogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9894	22642	35854	3.55	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10900	23580	36630	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11823	24484		4.16	1.1E-02	AA688239.1	EST_HUMAN	ab77f11.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:553005 3' similar to contains
12678	18829		1.62	1.1E-02	AA813796.1	EST_HUMAN	RC3-S10197-120200-015-g11 S10197 Homo sapiens cDNA
6	12833	25448	9.16	1.0E-02	AW848120.1	EST_HUMAN	MR3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA
1513	14260	26946	1.56	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
2577	15281		1.57	1.0E-02	AA806389.1	EST_HUMAN	cc22h08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3087	15652	28494	2.7	1.0E-02	BE835556.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3257	16019	28669	1.49	1.0E-02	BE868999.1	EST_HUMAN	80164967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933669 3'
3861	16611	29250	0.79	1.0E-02	AI066086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA

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3876	16626	29284	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
4728	17498	30084	4.24	1.0E-02	6753321	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr12), mRNA
4793	17524	30146	5.16	1.0E-02	R66567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5331	18134	30783	0.72	1.0E-02	H62881.1	EST_HUMAN	yq36h11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235941 5'
5881	18458	31370	0.37	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6025	18805	31766	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6088	18866	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MIR4-BT03568-070100-201-h01 BT03568 Homo sapiens cDNA
6088	18866	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MIR4-BT03568-070100-201-h01 BT03568 Homo sapiens cDNA
6664	19581	32616	1.92	1.0E-02	Z29642.1	NT	Z. mays U3snRNA pseudogene
9293	21960	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459670F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
9293	21960	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459670F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
11229	23892		1.97	1.0E-02	AF167659.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11263	23925		1.46	1.0E-02	AI417861.1	EST_HUMAN	ig55h07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1
11340	24030	37334	1.97	1.0E-02	AV760016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MIER6 repetitive element
12003	25416		1.83	1.0E-02	G62203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12059	25189	30811	3.78	1.0E-02	AW635521.1	EST_HUMAN	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12075	25243		5.93	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12592	25289		3.74	1.0E-02	X62654.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12803	25050	30957	1.84	1.0E-02	AB039887.1	NT	H sapiens gene for Me491/GD63 antigen
873	13642	26312	2.1	9.0E-03	AI796126.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
1241	13980		2.07	9.0E-03	BE781889.1	EST_HUMAN	wh4209.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2363433 3' similar to contains element MIER22
1463	14211	26889	1.1	9.0E-03	AE001270.1	NT	MER22 MIER22 repetitive element
2394	15115	27852	2.48	9.0E-03	AL161959.2	NT	601470242F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873346 5'
2403	15124	27861	0.92	9.0E-03	AF09934.1	NT	Treponema pallidum section 86 of 87 of the complete genome
3659	18412	29050	1.21	9.0E-03	J06184.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
4927	17855	30287	1.03	9.0E-03	BE047949.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
4984	17689	30287	0.95	9.0E-03	T70044.1	EST_HUMAN	S.acidocaldarius thermophilin gene, complete cds
4864	17689	30298	0.96	9.0E-03	T70044.1	EST_HUMAN	iz44e10.y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291466 5'
5720	18512		1.15	9.0E-03	AI809782.1	EST_HUMAN	yc17b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
6533	19289		4.88	9.0E-03	BE745988.1	EST_HUMAN	yc17b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
							wt7704.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
							601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'

Page 169 of 536  
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7362	20043	33122	0.57	9.0E-03	A1242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7371	20051	33132	0.8	9.0E-03	89222570	NT	Homo sapiens hypothetical protein FLJ10690 (FLJ10690), mRNA
7774	20470		1.05	9.0E-03	AL039891.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8147	20841		0.65	9.0E-03	AF223391.1	NT	
8745	22398	35601	0.47	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
9762	22413	35620	1.44	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10807	23587		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10935	23815	38868	1.57	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
11651	24248	37569	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.46	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-261299-001-c09 HT0452 Homo sapiens cDNA
							zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element
489	13274		4.06	8.0E-03	AA723007.1	EST_HUMAN	Homo sapiens edryosuccinate lyase gene, complete cds
968	13734	26399	36.32	8.0E-03	AF106658.1	NT	Homo sapiens chromosome 21 segment HS21G083
2184	14884	27617	2.2	8.0E-03	AL163283.2	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
2960	16726		0.93	8.0E-03	U47048.1	NT	Homo sapiens SCL gene locus
3353	18113	28768	1.08	8.0E-03	AJ131018.1	NT	
3665	18418	28058	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3665	18418	28069	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4350	17089	29721	4.88	8.0E-03	BF303327.1	EST_HUMAN	CMA-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5083	17802	30420	1.09	8.0E-03	AU140261.1	EST_HUMAN	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, leucine, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
8436	19235	30949	2.82	8.0E-03	AF110520.1	NT	
6108	25085	31852	1.45	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genome DNA, 287001-544000 nt position (2/7)
6661	19413	32427	4.89	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
8820	19481		0.95	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19795	32860	1.79	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
							BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
8781	21473	34819	0.63	8.0E-03	P98160	SWISSPROT	

Page 170 of 536  
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8808	21500	34646	3.28	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111189-011-h08 ST0111 Homo sapiens cDNA
8816	21508	34653	0.49	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
8878	21568	34713	0.58	8.0E-03	9789566	NT	Mus musculus fuslon 2 (human) (Fus2), mRNA
9848	22488		4.63	8.0E-03	BE088509.1	EST_HUMAN	QV1-BT0877-040400-131-g03 BT0877 Homo sapiens cDNA
10686	23357	36597	1.36	8.0E-03	BE788441.1	EST_HUMAN	60147681F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
10906	23586		3.58	8.0E-03	Z49682.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11715	24309	37632	4.74	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
11814	24402		22.71	8.0E-03	AA016180.1	EST_HUMAN	2a32e1.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380718 5'
11853	24437	37779	1.36	8.0E-03	BF342436.1	EST_HUMAN	602013941F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4149418 5'
11933	24491		1.74	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
11980	24523		1.74	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13483	26086	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
878	13483	26087	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
956	13721	26387	3.57	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1084	13882	26511	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.67	7.0E-03	Q81060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1374	14122	26787	6.71	7.0E-03	AA668288.1	EST_HUMAN	ab79b08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1491	14238	26924	3.37	7.0E-03	AW303599.1	EST_HUMAN	xv21b02.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27175	1.24	7.0E-03	AW950566.1	EST_HUMAN	EST1362626 MAGE resequences, MAGA Homo sapiens cDNA
1735	14477	27176	1.24	7.0E-03	AW950566.1	EST_HUMAN	EST1362626 MAGE resequences, MAGA Homo sapiens cDNA
2254	15589	27722	1.86	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3546	16301	28951	0.71	7.0E-03	AI150273.1	EST_HUMAN	q34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3749	16502	29137	0.8	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
3792	16544	29179	1.32	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4000	16502	29137	0.83	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4560	17296		1.24	7.0E-03	AW630888.1	EST_HUMAN	inh89a05.y1 NCI_CGAP_GL1 Homo sapiens cDNA clone IMAGE:2969338 5'
4929	17697		2.17	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5729	18521		0.76	7.0E-03	H71106.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6021	25083		4.9	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0288 Homo sapiens cDNA
6222	18986	31872	1.47	7.0E-03	W68251.1	EST_HUMAN	zs3310.r1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:342475 5'

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6443	18211	32207	3.44	7.0E-03	AA327129.1	EST_HUMAN	EST30874 Colon I Homo sapiens cDNA 5' end
6470	19237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	7934b10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6978	19504	32529	1.67	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384DB_2: contains TAR1:2 TAR1 repetitive element;
7420	20097	33184	5.48	7.0E-03	Z35938.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35938.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175697.1	EST_HUMAN	S. cerevisiae chromosome II reading frame ORF YBL077w
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9297	21864		0.75	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9495	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9620	22273	35460	2.57	7.0E-03	P48982	SWISSPROT	yv49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9620	22273	35461	2.57	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10204	22852		1.32	7.0E-03	AV687378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10384	23030		0.77	7.0E-03	AI769734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10729	23417	36658	2.63	7.0E-03	AB008852.1	NT	AV687378 GKCHomo sapiens cDNA clone GKCAFC07 5'
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10818	23601	36740	1.71	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
10982	23657		1.29	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12468	24853		1.79	7.0E-03	BE263263.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12553	24890		1.81	7.0E-03	Y17455.1	NT	Sporobolus stapianus mRNA for putative glycine and proline-rich protein
12691	25400		1.72	7.0E-03	AL163300.2	NT	601146164F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 6'
1218	13989	26837	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
1218	13989	26838	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment H321C100
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	hd22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2893	15660	28305	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW:PXN_HUMAN O79469 ORPHAN NUCLEAR RECEPTOR PXR;
2893	15660	28306	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW:PXN_HUMAN O79469 ORPHAN NUCLEAR RECEPTOR PXR;
3240	16002		2.22	6.0E-03	H75690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
3298	16060		1.31	6.0E-03	AF190338.1	NT	ah78e11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
3377	16136	28793	1.18	6.0E-03	U90880.1	NT	ah78e11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 6'
							Nolencus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
							Fugu rubripes zinc finger protein, (isobolcin, fatty acid binding protein, sepiapterin reductase and vasotocin
							genes, complete cds

Page 172 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3377	16136	28794	1.18	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3534	16230		1.19	6.0E-03	W37985.1	EST_HUMAN	zc13a11.1f Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3652	16405	28044	3.68	6.0E-03	BF510986.1	EST_HUMAN	UJ-H-B14-apm-c-06-O-UJ.at1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087764 3'
3682	16435	28079	1.08	6.0E-03	BE077358.1	EST_HUMAN	RC1-BT0608-280400-014-a07 BT0608 Homo sapiens cDNA
3759	16511	29147	1.22	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
3802	16652	28294	0.76	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
3838	16688		1.29	6.0E-03	BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4331	17070		1.84	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4847	17381	30073	5.67	6.0E-03	AA24242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5073	17792	30407	2.58	6.0E-03	Q82209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
6081	25084	31802	0.67	6.0E-03	9627521	NT	Varola virus, complete genome
6718	19633	32878	1.16	6.0E-03	O14894	SWISSPROT	SYNAPSIN III
6755	17924	30559	0.57	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	19836	32905	0.61	6.0E-03	AA298442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7149	19836	32906	0.61	6.0E-03	AA298442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7646	20216	33318	0.69	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7702	20365	33479	0.62	6.0E-03	P17684	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7767	20453	33578	6.9	6.0E-03	A033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1846670 3' similar to contains MER10.b1 MER10 repetitive element;
7874	20569	33695	2.17	6.0E-03	AW799337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7845	20840		1.58	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858628 5'
9454	22004	35176	7.26	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9943	22591		2.13	6.0E-03	A1432681.1	EST_HUMAN	tt22c02.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10062	22710	35928	0.86	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A;
10194	22842		1.14	6.0E-03	AF084555.1	NT	Bacillus subtilis fnd gene
10304	22951	35166	0.59	6.0E-03	X68386.1	NT	cds
10845	23336	35575	1.75	6.0E-03	AW902164.1	EST_HUMAN	Mt thermophilum complete plasmid pFV1 DNA
10713	23402		2.54	6.0E-03	11545814	NT	EST374237 MAGG sequences, MAGG Homo sapiens cDNA
10760	23435	36680	1.26	6.0E-03	A1420786.1	EST_HUMAN	Homo sapiens hypophyseal zinc finger protein FLJ14011 (FLJ14011), mRNA
							tt91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.;

Page 173 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23435	36881	1.26	6.0E-03	AI420786.1	EST_HUMAN	tes1c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
10903	23583		4.6	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10904	23584	36833	2.81	6.0E-03	BE737895.1	EST_HUMAN	601572748F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12042	24563		3.25	6.0E-03	AF070496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12160	25174		6.69	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 460298 (section 39 of 148) of the complete genome
12239	25235		3.17	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12669	24898		1.64	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12688	24910		1.68	6.0E-03	AJ245480.1	NT	Brassica napus s1a gene for S-locus glycoprotein, cultivar T2
654	13432	26072	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	13432	26073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocyclase synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1090	13848	26507	1.15	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2688	15397	28135	2.5	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2936	15702	28351	0.88	5.0E-03	BE266057.1	EST_HUMAN	601184786F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3133	15898	28543	3.82	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3152	15916		2.83	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3164	15927	28575	1.3	5.0E-03	R77794.1	EST_HUMAN	y86g02.s1 Soares breast 2N1Bb1 Homo sapiens cDNA clone IMAGE:155666 3'
3272	16033		1.12	5.0E-03	AJ297357.1	NT	Homo sapiens partial UMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3687	16440	28082	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3741	16494	28129	0.85	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3954	16704		1.17	5.0E-03	AA299975.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4272	16494	28129	0.82	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4569	17304	28931	0.73	5.0E-03	AJ131016.1	NT	Homo sapiens SCI gene locus
4670	17404	30039	1.17	5.0E-03	A752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn15c02 random
5707	18501	31422	5.5	5.0E-03	P335500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Page 174 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5953	18735	31894	2.97	5.0E-03	Q00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5988	18769		0.91	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 82 of 94 of the complete genome
6489	18264		7.56	5.0E-03	BE300091.1	EST_HUMAN	800944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660871 3'
6746	17915	30578	7.45	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6940	19422		0.64	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7385	20065	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFBOR63 similar to EST containing Alu repeat
7488	20170		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-07 CT0255 Homo sapiens cDNA
7667	20331	33442	7.5	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8119	20813	33948	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33985	3.29	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8509	21201		5.63	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 mln)
8838	21530	34878	0.71	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9482	22135	35315	0.45	5.0E-03	P33750	SWISSPROT	SOF-1 PROTEIN
9739	22390	35595	0.89	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9871	22521	35718	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA633143.1	EST_HUMAN	h46h70.s1 NCI CGAP Pr0 Homo sapiens cDNA clone IMAGE:985567
10231	22879	36091	0.51	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10377	23023		0.48	5.0E-03	AA653261.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126280 3'
10621	23314		4.99	5.0E-03	T16888.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	zn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040.3' similar to contains L1.12 L1 repetitive element;
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	zn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040.3' similar to contains L1.12 L1 repetitive element;
10971	23647	36900	1.89	5.0E-03	T49153.1	EST_HUMAN	yo99e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11021	23693	36958	1.47	5.0E-03	10948753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC88212), mRNA
11303	23962		3.54	5.0E-03	BE048055.1	EST_HUMAN	tz46e04.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
11774	24365	37697	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24365	37698	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12176	25367		9.26	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12409	24792		2.62	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-64, complete cds
12441	24811		1.67	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:808548 3' similar to
12467	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	SW/DXA2_MOUSE P14885 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12643	24940	30980	4.2	5.0E-03	AW449109.1	EST_HUMAN	90207774F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4232002 5'
12662	26263		1.76	5.0E-03	Q02388	SWISSPROT	UI-HB13-akf-08-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734216 3'
226	13038	25975	2.98	4.0E-03	AW500196.1	EST_HUMAN	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
313	13117	25755	2.28	4.0E-03	R48482.1	EST_HUMAN	UI-HF-BNO-akc-H-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
689	13369	26997	2.69	4.0E-03	AA939339.1	EST_HUMAN	y951a04.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:359883 3'
857	13628	26298	2.03	4.0E-03	R48482.1	EST_HUMAN	on75g12.s1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:1662568 3'
891	13660		4.84	4.0E-03	AW749101.1	EST_HUMAN	y951a04.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:359883 3'
1128	13884	26544	29.46	4.0E-03	AA099777.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1146	13901	26563	2.4	4.0E-03	AW794740.1	EST_HUMAN	z181a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:610998 5'
1280	14030	26699	1.57	4.0E-03	AA284374.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1581	14327		1.52	4.0E-03	AV708305.1	EST_HUMAN	zs59a01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1737	14479	27178	2.23	4.0E-03	U33472.1	NT	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
2011	14746	27474	10.66	4.0E-03	AA099777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
2244	14972		2.49	4.0E-03	BE410556.1	EST_HUMAN	z181a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2276	15002	27742	1.64	4.0E-03	AW794740.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2579	15293	28030	1.97	4.0E-03	U52111.2	NT	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2679	15293	28031	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2698	15403	28140	3	4.0E-03	AJ277365.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2696	15405	28141	3	4.0E-03	AJ277365.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3219	15982	28634	1.16	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens polyglutamine-containing C14ORF4 gene
3219	15982	28635	1.16	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens polyglutamine-containing C14ORF4 gene
3521	16277	28931	0.97	4.0E-03	AW189426.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
							PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
							x98f04.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'

Page 176 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3621	16277	28932	0.97	4.0E-03	AW188426.1	EST_HUMAN	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3612	16365	29008	0.73	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3909	16689	29300	0.73	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tag101) gene, complete cds
3977	16726		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5057	17776	30393	0.83	4.0E-03	AW103719.1	EST_HUMAN	xe83d03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1.t1 L1
5114	17832		0.97	4.0E-03	AA772898.1	EST_HUMAN	L1 repetitive element;
5194	18002	30625	1.8	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-calenin binding protein mRNA, complete cds
5705	18499	31421	2.48	4.0E-03	P04186	SWISSPROT	(HPRG)
5708	18502	31423	1.74	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
5792	18583	31510	0.88	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7811014_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014 5'
5993	18774		4.11	4.0E-03	U22180.1	NT	Rattus norvegicus opsh gene, complete cds
6140	18918	31888	0.95	4.0E-03	AW590572.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2848652 3'
6217	18991	31897	1.6	4.0E-03	BE548453.1	EST_HUMAN	601076076F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461864 5'
6572	19336	32347	1.28	4.0E-03	AA813222.1	EST_HUMAN	aj32f11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
6877	19594	32632	1.61	4.0E-03	U76408.1	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	18787	32851	3.5	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7331	20013	33091	1.23	4.0E-03	AI681483.1	EST_HUMAN	b37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7393	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7424	20101		0.74	4.0E-03	X92109.1	NT	H. sapiens hcgIX gene
7843	20538	33666	0.7	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 6)
7947	20642	33767	5.45	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS6) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8103	20797	33928	2.06	4.0E-03	7662087	NT	Dichytellum discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8614	21306	34448	6.98	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8787	21479		4.25	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9827	22478	35879	0.87	4.0E-03	H30694.1	EST_HUMAN	yp42g12.11 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10276	22923	36135	1.3	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
10466	23112		0.45	4.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Page 177 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11074	23744	37017	4.09	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21, segment HS21C006
11777	24368	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	26386		1.78	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12167	24649		2.38	4.0E-03	BE288280.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12246	24684		2.27	4.0E-03	AW504273.1	EST_HUMAN	UHF-BN0-alp-9-04-UJ1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	Tq74c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12521	25293		2.08	4.0E-03	AW614598.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2963932 3' similar to contains element LTR5 repetitive element;
12801	26048	30868	2.17	4.0E-03	11438956	NT	Homo sapiens Grb2-associated binder 2 (KIAA0671), mRNA
362	13160	25803	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26289	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14982		1.38	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2292	15017		6.44	3.0E-03	Z32621.1	NT	S.cereale (cv. Haio) mRNA for triosephosphate isomerase
2293	15018	27753	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
2293	15018	27754	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
3081	15846	28488	3.31	3.0E-03	BE376296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5'
3149	15912	28557	2.52	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA
3412	16170	28819	1.72	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3420	16177		5.87	3.0E-03	Y12500.1	NT	C.elegans samdc gene
3959	16708	29348	6.97	3.0E-03	AV782392.1	EST_HUMAN	AV782392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3959	16708	29349	6.97	3.0E-03	AV782392.1	EST_HUMAN	AV782392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4016	16782	29380	1.35	3.0E-03	A1792278.1	EST_HUMAN	ah04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4130	16872		1	3.0E-03	Z32521.1	NT	S.cereale (cv. Haio) mRNA for triosephosphate isomerase
4364	17102	29737	6.63	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdhf gene
4428	17184		0.73	3.0E-03	BE348739.1	EST_HUMAN	hfb8g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4482	17217	28844	4.97	3.0E-03	AI638141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4782	17514	30136	2.38	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4802	17533	30165	7.94	3.0E-03	BE787045.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5184	17992	30508	3.98	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5468	18267	31159	1.98	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)

Page 178 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5639	18337	31244	0.99	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	19225	32225	11.75	3.0E-03	AA466701.1	EST_HUMAN	aa13f10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19792	32857	1.38	3.0E-03	AJ011418.1	NT	Kluyveromyces marxianus pep3 gene for purine-cytosine permease
7422	20099	33187	3.84	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7839	20534	33861	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250800-032-e07 BT0812 Homo sapiens cDNA
7839	20534	33662	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250800-032-e07 BT0812 Homo sapiens cDNA
8056	20750	33881	1.54	3.0E-03	N92880.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NHPA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20908		0.51	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8360	21053	34184	1.32	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8381	21074	34213	1.47	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8485	21177		1.29	3.0E-03	Q8QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8890	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.t1 L1 repetitive element;
8943	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8967	21657	34808	6.44	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X67138_ma1 HISTONE H2B.2 (HUMAN);
8977	21687	34817	0.73	3.0E-03	BF338078.1	EST_HUMAN	60203580F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4189898 5'
9309	21976		0.83	3.0E-03	D90901.1	NT	Synedococcus sp. PCC6803 complete genome, 3/27, 271600-402289
9347	20418	33538	0.83	3.0E-03	BE154670.1	EST_HUMAN	PM3-HT0344-071289-003-d07 HT0344 Homo sapiens cDNA
9538	22189		0.54	3.0E-03	P03355	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9608	22259		3.98	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROITE PROTEIN PRECURSOR (CS)
9795	22446	35651	1.3	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9896	22546	35740	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10040	22688	35906	3.97	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10762	23437		1.8	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11137	20099	33187	2.65	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11363	24043	37346	1.69	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11424	23191	36422	2.52	3.0E-03	AF268285.1	NT	Homo sapiens globin-like protein (GLP) gene, complete cds
11462	24065	37372	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11462	24065	37373	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.58	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

Page 179 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW294812.1	EST_HUMAN	UI-H-BJ2-ah4-08-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
11927	25186		2.86	3.0E-03	AI925056.1	EST_HUMAN	promina-5.E07.r bvtumor Homo sapiens cDNA 5'
11982	24510	37256	1.88	3.0E-03	AA993154.1	EST_HUMAN	ct7b10.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;
12016	25321		2.26	3.0E-03	AB009688.1	NT	Homo sapiens gene for GMP-N-acetylneuraminic acid hydroxylase, partial cds
12180	24661	31068	2.71	3.0E-03	AI296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
502	13288	25919	1.83	2.0E-03	Q04952	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03	Q04952	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	18552		12.31	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108341 5'
1342	14090	26766	2.07	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1345	14083	26768	1.4	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCL_CGAP_AlV1 Homo sapiens cDNA clone IMAGE:1217693
1354	14102	26777	16.16	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26906	1.73	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1506	14252	26938	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1586	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1784	14506	27207	1.13	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061089-018-d03 HT0183 Homo sapiens cDNA
1888	14724	27446	1.57	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.16	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15288		4.57	2.0E-03	AW137782.1	EST_HUMAN	UI-H-BI1-adi-g-10-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF668955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3667	16410	29048	6.62	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 8, 13 and 14 genes
4093	16835	29461	1.96	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4195	16938		11.03	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4393	17130		1.12	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-air-g-03-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4397	17134	29765	0.97	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4609	17244	29877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlegged class 2 (shc) mRNA, complete cds
4509	17244	29878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlegged class 2 (shc) mRNA, complete cds
4663	17397		1.84	2.0E-03	R87773.1	EST_HUMAN	yo45a02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4956	17682	30290	2.57	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5092	17811	30427	1	2.0E-03	BE798380.1	EST_HUMAN	601863004F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937680 5'
5399	18189	30893	1.38	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5540	25070	31245	2.08	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0893 protein, partial cds
5623	18420	31333	1.86	2.0E-03	U63711.1	NT	Xenopus laevis xerilin mRNA, complete cds
6019	18800	31760	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6253	19027	32002	2.17	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6255	19029	32004	7.6	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6291	19064	32046	2.44	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19065	32047	0.98	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6320	19090	32078	1.62	2.0E-03	X94451.1	NT	L.esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6508	19271		1.16	2.0E-03	AI991083.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
6541	19306	32311	0.91	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
6862	17939	30576	1.52	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6939	19674	32720	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
6939	19674	32721	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
6981	19506	32531	3.65	2.0E-03	BE067988.1	EST_HUMAN	C1V4-BT0368-051289-054-d01 BT0366 Homo sapiens cDNA
7044	19735	32785	0.98	2.0E-03	AI299883.1	EST_HUMAN	qm89d11.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1898885 3'
7193	19879	32953	0.8	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares_fetal_liver spleen_INFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7617	20188	33281	1.18	2.0E-03	P07364	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7950	20645	33769	1.96	2.0E-03	AW592004.1	EST_HUMAN	m87b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY.;
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element;

Page 181 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares melanocyte 2NbrIM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element:
8162	20856	33987	0.54	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.09 IN CHROMOSOME 1
8184	20876	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20933	34069	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	34070	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8284	20958	34087	0.86	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8318	21011		0.91	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21262	34400	0.54	2.0E-03	AB035256.1	NT	Oxytrogus culiculus mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0026 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9139	21827	34992	0.64	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9426	22104	35276	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194286 3'
9426	22104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194286 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JLI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9458	22008	35178	3.46	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9566	22219	35404	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9566	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35484	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9823	22276	35485	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22486	35568	0.81	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
9942	22590		5.75	2.0E-03	AA251376.1	EST_HUMAN	z310a06.s1 NCL CGAP GCBI Homo sapiens cDNA clone IMAGE:684764 3'
10508	23162	36377	0.45	2.0E-03	AW361178.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10508	23162	36378	0.45	2.0E-03	AW361178.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10938	23618	33281	2.97	2.0E-03	M86524.1	NT	Human dystrophin gene
11470	24131		2.56	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11538	24138	37446	9.1	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
							(y65103.x1 NCL CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25932 VACUOLAR ATP SYNTHASE SUBUNIT G;
11809	24473		3.23	2.0E-03	A1625745.1	EST_HUMAN	Homo sapiens SEL1L (SEL1L) gene, partial cds
11926	24487	37807	2.41	2.0E-03	AF157516.2	NT	

Page 182 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11849	24502	37810	2.41	2.0E-03	AI084325.1	EST_HUMAN	oy43g06.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to TR:P97635 P97635 PS-PLA1 PRECURSOR. ;
11972	17907		9.37	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12172	25361		2.99	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
12282	24707	31050	1.78	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12433	26224		1.48	2.0E-03	AI375037.1	EST_HUMAN	ta66f02.x1 Soares_total_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element
12542	24882		1.64	2.0E-03	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT6, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12713	25175		2.65	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
429	13215	26860	1.28	1.0E-03	H98471.1	EST_HUMAN	y98c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
810	13681	26248	2.31	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
810	13681	26249	2.31	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
1073	13831	26489	3.78	1.0E-03	AI865788.1	EST_HUMAN	wa86a06.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422268 3'
1083	13851	26510	1.78	1.0E-03	AI954572.1	EST_HUMAN	wx93e10.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2021	14756	27488	3.38	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2150	14880	27614	12.13	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2979	15745	28393	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3186	15949	28598	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3186	15949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3656	19409		1.65	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4402	17139	29767	1.28	1.0E-03	BE938162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4441	17177	29803	4.05	1.0E-03	BE246536.1	EST_HUMAN	TCBAP-ID4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4616	17360	29985	0.84	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4773	17505	30127	1.68	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4773	17505	30128	1.68	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4774	17508		4.29	1.0E-03	BE154067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5018	17739	30348	7.24	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5225	18032	30558	1.87	1.0E-03	AA280951.1	EST_HUMAN	zs44f01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5369	18170	30856	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5369	18170	30857	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5485	18284	31182	0.83	1.0E-03	BE796491.1	EST_HUMAN	60188941F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5491	18280	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5546	18343	31251	0.67	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270597 5' similar to contains element MER8 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270597 5' similar to contains element MER8 repetitive element;
5930	18714		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5968	18760	31711	1.07	1.0E-03	BE983639.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6099	18877	31990	8.78	1.0E-03	T87781.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6242	19016		1.14	1.0E-03	T87781.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:115772 5'
6315	18086		1.7	1.0E-03	AW902585.1	EST_HUMAN	QV3:NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6657	19418	32432	1.37	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7052	19743	32805	2.54	1.0E-03	D16628.1	NT	Human gene for fourth somatostatin receptor subtype
7539	20209	33308	1.8	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7608	20274	33382	3.37	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7658	20320	33429	0.98	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 6'
7789	20484	33608	0.83	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7850	20545	33673	5.18	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerh-1 gene
8043	20737	33870	1	1.0E-03	AA122270.1	EST_HUMAN	z497c09.s1 Soares_pregnant_uterus_NHPIU Homo sapiens cDNA clone IMAGE:480788 3' similar to contains L1.11 L1 repetitive element;
8142	20836	33868	1.94	1.0E-03	AF153880.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8329	21022	34158	0.68	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8492	21184	34326	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8842	21534		1.36	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxopsin
8889	21560	34705	0.62	1.0E-03	AW840363.1	EST_HUMAN	CNM3-LT0078-170200-092-e07 LT0078 Homo sapiens cDNA

Page 184 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		0.58	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrioleukodystrophy protein >
9017	21707	34858	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9017	21707	34859	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9507	22160	35340	1.66	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,8-galactosidase (aglA) gene, complete cds
9507	22160	35341	1.66	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,8-galactosidase (aglA) gene, complete cds
9720	22371	35570	0.81	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10063	22711	35929	0.65	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10066	22716		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10214	22862	35075	1.72	1.0E-03	A024350.1	EST_HUMAN	ov5708.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
10503	23149		0.46	1.0E-03	AA708202.1	EST_HUMAN	ag93f1.2.g1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:1142083 3' similar to contains Alu repetitive element;
10563	23259	36495	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10563	23259	36498	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10651	23342	36580	2.78	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
10726	23413		3.29	1.0E-03	A1583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248448 3' similar to TR:Q26185 Q26185 PVA1 GENE.;
10808	23491	36727	1.36	1.0E-03	AW237482.1	EST_HUMAN	xm72d12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2689751 3'
11106	23776		3.05	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11905	24470	37805	4.48	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12124	24616		1.38	1.0E-03	AV731520.1	EST_HUMAN	AV731520 HTF Homo sapiens cDNA clone HTFAUG05 5'
12371	25342		1.88	1.0E-03	A1347355.1	EST_HUMAN	lc05h11.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12478	25365	30612	7.05	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12821	25187	30809	1.37	1.0E-03	AW847341.1	EST_HUMAN	RC0-CT0205-240899-021-a02 CT0205 Homo sapiens cDNA
5130	17848	30465	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5596	18391		1.26	9.0E-04	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6185	18942		0.6	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6395	19184	32185	0.98	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
9543	22186		1.42	9.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgBAST mRNA for beta-amyrin synthase, complete cds
1471	14218		1.02	8.0E-04	X99469.1	NT	X.laevis mRNA for C4SR protein

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4159	18899		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.83	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11268	23928		1.98	8.0E-04	A1571093.1	EST_HUMAN	tr85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119	27856	0.97	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	15428	28184	1.19	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3274	16035	28685	1	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 9 (GXORF9) mRNA
6005	18786	31748	0.84	7.0E-04	AA518212.1	EST_HUMAN	rg65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1
6420	18188		2.47	7.0E-04	A1789331.1	EST_HUMAN	repetitive element;
7128	19818		0.78	7.0E-04	AK022445.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
9703	22354	35549	0.53	7.0E-04	P13487	SWISSPROT	Homo sapiens mRNA for FLJ00335 protein, partial cds
9703	22354	35550	0.53	7.0E-04	P13487	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24156		2.28	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11586	24185	37500	4.04	7.0E-04	240561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and F1P3 (F1P3) genes, complete cds
12642	24939		2.31	7.0E-04	R17336.1	EST_HUMAN	HSC2BA072 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:32298 5'
12689	24964		5.98	7.0E-04	6005855	NT	yg13c06.f1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
3941	16691	28328	1.83	6.0E-04	A1862525.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4088	16812	29440	0.78	6.0E-04	K01315.1	NT	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4088	16812	29441	0.78	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4162	16502	28531	3.79	6.0E-04	U45983.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
7478	20181	33245	0.61	6.0E-04	Q15034	SWISSPROT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7765	20461		3.33	6.0E-04	P46408	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7914	20609		0.62	6.0E-04	H92947.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
9880	22530		3.5	6.0E-04	AL048507.2	EST_HUMAN	y84c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains
9980	22828	35837	2.28	6.0E-04	BE005850.1	EST_HUMAN	LOR1 repetitive element;
10238	22866		0.71	6.0E-04	AF287478.1	NT	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
11467	24070	37378	2.53	6.0E-04	AJ226042.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11568	24157	37467	3.46	6.0E-04	AW013947.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11638	24233		2.17	6.0E-04	Q01768	SWISSPROT	U1-HBJ0-eab-e-09-QJUI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708826 3'
12082	25249		2.81	6.0E-04	AW380519.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
							RC1-HT0269-281189-012-c08 HT0269 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12816	25058		1.34	6.0E-04	AI817088.1	EST_HUMAN	w76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
636	13415	26051	6.81	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
1490	14237		1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3408	16166	28815	1.35	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element
3704	16457	29086	2.32	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5388	18188	30877	2.99	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6532	19298	32303	7.89	5.0E-04	AA158080.1	EST_HUMAN	z333b08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
7276	19960	33037	3.75	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7858	20551	33677	5.2	5.0E-04	AI188382.1	EST_HUMAN	qd1306.x1 Soares_placenta_8bc8weeks_ZNbpH8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;
8202	20896	34033	0.96	5.0E-04	AA814519.1	EST_HUMAN	cb96e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9177	21847	35013	1.39	5.0E-04	AA846545.1	EST_HUMAN	ej56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9271	22025	35195	0.88	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9418	22096	35258	1.44	5.0E-04	P29128	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9509	22162	35344	4.1	5.0E-04	AW270938.1	EST_HUMAN	xs08e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10177	22826		0.48	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
10897	23577		2.38	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_1 586 (synonym: hule7) Homo sapiens cDNA clone DKFZp586M2024
11713	18186	30877	14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12020	25184		5.04	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.e1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:913875
658	13435	26076	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26287	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ;
827	13597	26288	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ;
1449	14196	26880	3.18	4.0E-04	AW753396.1	EST_HUMAN	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2076	14807	27538	1.81	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 187 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2129	14860		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
2633	15345	28088	2.21	4.0E-04	O98815	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.95	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	29853	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4289	17028	29854	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4500	17236	28868	1.76	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:582670 3'
5028	17748	30360	3.1	4.0E-04	BE560860.1	EST_HUMAN	601345895F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3878910 5'
7168	18855	32925	1.3	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	AL161568.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7618	20284	33394	0.56	4.0E-04	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8434	21127	34264	1.07	4.0E-04	BF240712.1	EST_HUMAN	601876985F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4099700 5'
8442	21134	34270	1.5	4.0E-04	N25507.1	EST_HUMAN	yx38e12.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:284142 5'
9500	22243	35426	3.24	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
9740	22391		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(al7) mRNA, alternatively spliced, complete cds
12380	25157		2.05	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
152	12967	25508	3.46	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
180	13003	25844	2.24	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
860	13629	26300	1.32	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1831	14570	27282	1.08	3.0E-04	AI262100.1	EST_HUMAN	qt28d03.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1846	14584		1.21	3.0E-04	A398674.1	EST_HUMAN	fh23a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3303	16064	28712	3.43	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3308	16068	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	z66a04.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478 5'
3846	16698	28335	4.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779		1.33	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4072	16816		1.12	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
4766	17498		4.72	3.0E-04	BE163778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4827	17558	30180	0.95	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
5063	17782	30399	0.96	3.0E-04	AA613145.1	EST_HUMAN	nc08g09.s1 NCL CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1143328 3'
6062	18832		7.86	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6722	18556	32586	2.82	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7491	20163	33256	0.84	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

Page 188 of 536  
Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20851	33983	3.23	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	z48408.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10078	22726	35943	0.65	3.0E-04	A1992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w76a1.1.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10356	23003	36220	3.73	3.0E-04	AA781201.1	EST_HUMAN	a124g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
10495	23141	36387	0.54	3.0E-04	P13816	SWISSPROT	RIBOSOMAL PROTEIN L7A (HUMAN);
11595	24184	37466	1.38	3.0E-04	4501960	NT	GLUTAMIC ACID-RICH PROTEIN PRECURSOR
11976	25396	30617	4.81	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens adrenolegic, alpha-1A-, receptor (ADRA1A), mRNA nc38e04.r1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element 1;
12338	25230	30818	3.08	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
12730	25000		2.75	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547L185 5'
171	12984	25624	2.65	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helix-coiled-coil protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
466	13251	25692	1.8	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
887	13656	26324	10.71	2.0E-04	M86524.1	NT	Human dystrophin gene
887	13658	26325	10.71	2.0E-04	M86524.1	NT	Human dystrophin gene
1156	13911		3.93	2.0E-04	AI286021.1	EST_HUMAN	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element 1;
1163	13917		2.18	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1824	14563		1.12	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pib3 gene
2581	15295	28033	4.47	2.0E-04	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
2988	15762	28398	1.11	2.0E-04	AI124529.1	EST_HUMAN	am56c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3'
3328	16088	28740	1.1	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3429	16188	28834	1.99	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3892	16642	29282	0.79	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences; MAGP Homo sapiens cDNA
4122	16894		4.93	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4620	17355	29990	1.74	2.0E-04	H96285.1	EST_HUMAN	y0101r1.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4620	17355	29991	1.74	2.0E-04	H96285.1	EST_HUMAN	y0101r1.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4742	17474		1.63	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4988	17721	30324	1.1	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds

Page 189 of 536  
Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5089	17808	30424	1.04	2.0E-04	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHG)
5457	18256	31146	0.73	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5469	18268	31160	1.75	2.0E-04	AI680862.1	EST_HUMAN	IQ03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
5664	18459	31373	0.96	2.0E-04	AA286652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
5857	18844	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6144	18922	31892	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	19818		2.6	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7229	19910		0.55	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33295	1.42	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (166 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33676	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20878	34012	1.23	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20878	34013	1.23	2.0E-04	AB026899.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8453	21155	34298	1.96	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8642	21334	34478	0.49	2.0E-04	X67331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9233	21812	35086	0.49	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.st Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9319	21886	35158	0.6	2.0E-04	P18775	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGFG26.1
9875	22525	35719	1.19	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
9916	22565	35761	1.77	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864 5'
10755	23440	36684	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11128	23796		1.61	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 6
11276	23937	37229	3.06	2.0E-04	AJ440282.1	EST_HUMAN	ij011f1.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
11403	24052	37356	2.86	2.0E-04	AW136740.1	EST_HUMAN	UI-H-B11-adim-c-04-Q-UJ.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
11857	24441	37782	2.77	2.0E-04	AB21304.1	EST_HUMAN	yf79b10.x5 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77371 3'
1053	13812	28472	3.3	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1092	13850	28508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1092	13850	28509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

Page 190 of 536  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 88 gene, partial cds; and ORF 89, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 88 gene, partial cds; and ORF 89, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
3278	18039	28889	1.06	1.0E-04	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3719	18472	29110	0.91	1.0E-04	A1440282.1	EST_HUMAN	J01111.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4037	18782	29412	2.11	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4062	18807	29437	1.15	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC8BD04 3'
5036	17755	30368	1.28	1.0E-04	7662016	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31556	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
5834	18623	31557	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.99	1.0E-04	AA177111.1	EST_HUMAN	nc02et12.s1 NCL_CGAP_P33 Homo sapiens cDNA clone IMAGE:252
6738	19572	32605	0.92	1.0E-04	AA694591.1	EST_HUMAN	h125a04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97262
7086	19776	32841	15.6	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7470	19776	32841	17.82	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1885683 3'
7894	20689	33719	0.95	1.0E-04	AA630463.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1885683 3'
9236	21915	35088	2.27	1.0E-04	A1806220.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854664 3'
9247	21926	35097	1.46	1.0E-04	O88959	SWISSPROT	mf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9325	21992	35381	0.49	1.0E-04	T77163.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN B)
9546	22189	35381	1.66	1.0E-04	10863878	NT	yd72c08.r1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:113774 5'
10079	22727		2.74	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04	M28587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11567	24166	37479	2.05	1.0E-04	AW205336.1	EST_HUMAN	Mouse alpha leukocyte interferon gene, complete cds
11567	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	UI-H-B11-sew-a-02-q-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11649	24246	37566	1.76	1.0E-04	AB032968.1	NT	UI-H-B11-sew-a-02-q-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
							Homo sapiens mRNA for KIAA1142 protein, partial cds

Page 191 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11682	24287	37609	2.01	1.0E-04	AW269081.1	EST_HUMAN	xv49g12.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11725	24319	37643	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11725	24319	37644	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE678399.1	EST_HUMAN	7f29a10.x1 NCI_CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1 repetitive element;
682	13457	26102	2.76	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1282468 3'
1897	14733	27455	1.14	9.0E-06	AW899218.1	EST_HUMAN	QV4-SN0023-070400-166-b04 SN0023 Homo sapiens cDNA
5873	18660	31601	1.81	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33242	0.6	9.0E-05	AW204958.1	EST_HUMAN	UJH-B11-aer-d-05-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7476	20149	33243	0.8	9.0E-06	AW204958.1	EST_HUMAN	UJH-B11-aer-d-05-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9376	21851		3.02	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
9376	21853	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11082	23752	37027	2.68	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Bri8 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11207	23870	37156	1.75	9.0E-05	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982436 3' similar to contains element
11617	18660	31601	3.5	9.0E-05	Q60716	SWISSPROT	MIR repetitive element; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12176	26259		6.63	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G5b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
802	13574	26237	1.97	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
844	13614		2.75	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2950	15718		0.73	8.0E-05	M83576.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4448	17194	29808	0.87	8.0E-05	AW044605.1	EST_HUMAN	wv78a04.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
11099	23789	37045	1.84	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12765	25242		4.65	8.0E-05	AA278933.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSRT1 repetitive element;
337	13138	25773	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
337	13138	25774	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
554	13337	25965	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foera cDNA Homo sapiens cDNA clone EST HFD072014
554	13337	25966	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foera cDNA Homo sapiens cDNA clone EST HFD072014
1033	13793	26453	1.4	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2724	19431	28168	2.89	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 192 of 536  
Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3156	15919	28565	5.72	7.0E-05	AB009080.1	NT	Dictyostellium discoideum gene for TRFA, complete cds
4339	17078	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17149	29776	0.95	7.0E-05	U6080.1	NT	Caenorhabditis elegans Slp1p homolog mRNA, complete cds
4871	17598	30221	0.71	7.0E-05	9845300	NT	Rat cytomegalovirus Maasricht, complete genome
8124	20818	33954	1.09	7.0E-05	AA505582.1	EST_HUMAN	h93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:886086 3'
8453	22003	35175	2.97	7.0E-05	T07085.1	EST_HUMAN	EST04984 Fetal brain, Stragene (cat#838208) Homo sapiens cDNA clone HFBED60
11112	23782		3.09	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2020	14755	27484	1.89	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2020	14755	27485	1.89	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2595	15309	28048	1.19	8.0E-05	AI655241.1	EST_HUMAN	wb54h08.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2690	15399	28137	1.1	8.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2690	15399	28138	1.1	8.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2817	13440	26080	3.07	8.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5822	18811	31541	3.61	8.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5822	18811	31542	3.61	8.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6309	19081	32068	1.4	8.0E-05	N12829.1	EST_HUMAN	y50g11.r1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:248212 5'
6834	19496	32520	0.95	8.0E-05	AA897880.1	EST_HUMAN	q80a03.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
7983	20678	33803	0.76	8.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
7983	20678	33804	0.76	8.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
8342	21035	34172	0.62	8.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8347	21040	34177	2.22	8.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8479	21171	34316	0.63	8.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9151	21882	35050	1.21	8.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9151	21882	35051	1.21	8.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9421	22099	35271	0.85	8.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:118062 5'
9621	22274	35462	0.59	8.0E-05	AW627985.1	EST_HUMAN	h37a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10649	23340	36579	3.08	8.0E-05	R76639.1	EST_HUMAN	y59d08.s1 Soares_placenta_Nb2-IP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
11502	24103	37415	3.36	8.0E-05	AA044015.1	EST_HUMAN	zk56f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12387	25239	30822	14.34	8.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
12810	25053		1.4	8.0E-05	BE888403.1	EST_HUMAN	7g28a08.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307766 3'
1382	14129	26802	10.46	8.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 S T0234 Homo sapiens cDNA

Page 193 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1855	14593		1.2	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2851	15266	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3661	16710	28350	2.41	5.0E-05	AJ251884.1	NT	Homo sapiens partial SL C22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17793	30408	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17793	30409	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6003	18688	31639	3.75	5.0E-05	AV65344.1	EST_HUMAN	AV65344 GLC Homo sapiens cDNA clone GLCDMA06 3'
6078	18853	31822	0.99	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19816		0.87	5.0E-05	AB037964.1	NT	Mus musculus gene for catenin, exon 1
12176	24810		3.84	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4449	17185	29809	0.73	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	29810	0.73	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
9841	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9423	22101		7.57	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9901	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10306	22853	36168	0.59	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10668	23359	36599	4.18	4.0E-05	AW627848.1	EST_HUMAN	h36c07.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element ;
12140	24829		1.48	4.0E-05	AW117680.1	EST_HUMAN	xd93e09.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805182 3'
12789	25041		1.71	4.0E-05	AA417768.1	EST_HUMAN	zv01e11.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:748252 3'
665	19441	28082	1.6	3.0E-05	A1248081.1	EST_HUMAN	q184c10.x1 Scarses_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1037	13797	28457	0.86	3.0E-05	AW279851.1	EST_HUMAN	xz24g03.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1109	13866	26523	1.01	3.0E-05	BF037988.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1109	13866	26524	1.01	3.0E-05	BF037988.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
3287	16048		0.73	3.0E-05	AI288918.1	EST_HUMAN	q191g11.x1 Scarses_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4349	17088	28719	7.98	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4349	17088	28720	7.98	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
							PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	29798	0.94	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4434	17170	29799	0.94	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4550	17285		0.99	3.0E-05	AL169302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4686	17420	30055	1	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	26082	0.82	3.0E-05	A1248061.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
4791	17622	30144	0.97	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002073 5'
5470	18269	31181	1.66	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6659	18419	32433	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6659	18419	32434	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7789	20494	33616	2.33	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8250	20944	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8791	21483	34630	1.59	3.0E-05	AW770982.1	EST_HUMAN	h184e08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009898 3'
8795	21487	34633	1.23	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8789	21491	34638	0.51	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9029	21719		0.56	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21899	35068	1.22	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Odon adenocarcinoma IV Homo sapiens cDNA 5' end
9563	22216		2.92	3.0E-05	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10433	23079	36303	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24585		1.77	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2323	15048	27784					q189e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15301	28037	1.09	2.0E-05	A1286021.1	EST_HUMAN	MER3.b2 MER3 repetitive element;
			2.43	2.0E-05	M13782.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2718	15425		7.46	2.0E-05	AA160562.1	EST_HUMAN	zq48a12.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3134	15699	28544	1.23	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3343	18102	28764	0.93	2.0E-05	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3362	18121	28779	1.22	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3485	18242		0.71	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3787	16539		0.78	2.0E-05	AL039107.1	EST_HUMAN	DKFZp568i064_r1 568 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp568i064 5'
4643	17377		1.08	2.0E-05	BE378471.1	EST_HUMAN	601238456F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808853 5'
5672	18487	31382	1.92	2.0E-05	AJ011712.1	NT	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)

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## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18616		0.69	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
5880	18669	31608	0.76	2.0E-05	Q19183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
5880	18666	31607	0.78	2.0E-05	Q19183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6065	18844	31808	0.61	2.0E-05	A1149272.1	EST_HUMAN	qz72a02.x1 Soares_placenta_8to9weeks_2NbHP8b9w Homo sapiens cDNA clone IMAGE:1715114 3'
6527	19293	32297	2.28	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.18 L1 repetitive element ;
6801	19462	32483	3.27	2.0E-05	Y08926.1	NT	hw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6814	19476	32497	1.12	2.0E-05	A1492960.1	EST_HUMAN	P. falciparum mRNA for AARP1 protein, partial
6824	19485		9.37	2.0E-05	A1991025.1	EST_HUMAN	qz47f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
7053	19744	32806	1.93	2.0E-05	AF224262.1	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ; wu35f07.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
7053	19744	32807	1.93	2.0E-05	AF224262.1	NT	Heterodontus fransdel HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA8 (HoxA8), HoxA6 (HoxA6), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7287	19951		0.83	2.0E-05	AF128847.1	NT	Heterodontus fransdel HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA8 (HoxA8), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7785	20480	33605	1.71	2.0E-05	A981040.1	EST_HUMAN	Homo sapiens indolethylamine N-methyltransferase (NMT) mRNA, INMT-2 allele, complete cds
9020	21710	34862	0.53	2.0E-05	BE244840.1	EST_HUMAN	ig20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9020	21710	34863	0.53	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1990 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1990
9167	21837	35002	0.58	2.0E-05	P49457	SWISSPROT	TCBAP2E1990 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1990
9167	21837	35003	0.58	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9823	22474	35677	0.49	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10035	22693	35900	0.67	2.0E-05	BF055339.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10457	23103	36333	0.54	2.0E-05	AJ131024.1	NT	7175g08.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5'
10457	23103	36334	0.54	2.0E-05	AJ131024.1	NT	Homo sapiens class gene, exon 1-alpha
10489	23135	36362	1.98	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens class gene, exon 1-alpha
10489	23135	36362	1.98	2.0E-05	N41751.1	EST_HUMAN	hw91a06.r1 Soares_placenta_8to9weeks_2NbHP8b9w Homo sapiens cDNA clone IMAGE:259570 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10489	23135	36363	1.98	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2Nb1P8b0W Homo sapiens cDNA clone IMAGE:269670 5'
10541	16485		2.42	2.0E-05	A1991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11287	23948	37243	1.33	2.0E-05	A1493285.1	EST_HUMAN	h30h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ;
11287	23948	37244	1.33	2.0E-05	A1493285.1	EST_HUMAN	h30h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ;
11430	23197	36428	2.27	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12185	25168		4.96	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3163532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2 ;
12342	25155		2.27	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12674	25247		1.44	2.0E-05	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
2266	14891	27731	3.22	1.0E-05	P27448	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
2700	15603	28143	1.6	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3641	16394	28034	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3793	16545		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3949	16899	28337	9.2	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4152	16894	28623	1.2	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4244	16985	28608	2.52	1.0E-05	AA431119.1	EST_HUMAN	zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4789	17330	30152	1.81	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2866548 3'
6653	19415	32428	1.22	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
6980	19505	32530	2.58	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element ;
6992	19875	32722	3.28	1.0E-05	4605844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7677	20341		1.16	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8813	21505		2.24	1.0E-03	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8938	21649	34789	3.02	1.0E-05	AA462578.1	EST_HUMAN	zd65h12.s1 Soares_tetral_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:U02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9187	21857	35022	12.45	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element ;
9266	22020	35189	0.62	1.0E-05	AV732180.1	EST_HUMAN	AV732180 HTF Homo sapiens cDNA clone HTFBIH01 5'
9738	22399	35593	0.74	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR.t1 OFR repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	22389	35594	0.74	1.0E-05	AW510802.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR11 OFR repetitive element;
9816	22467	35669	1.16	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9816	22467	35670	1.16	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW468995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
10836	23518	36760	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10836	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11854	24438	37780	1.38	1.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2678	16387	28129	4.8	9.0E-06	AI683811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3092	16857	28498	3.53	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_81c9weeks_2NbhPb9w Homo sapiens cDNA clone IMAGE:1759191 3'
3597	18350		2.82	9.0E-06	MB1755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5815	18604	31532	2.61	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 6, 8
6765	19509	32534	0.8	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7340	20021	33099	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7673	20337	33450	13.94	9.0E-06	AI034370.1	EST_HUMAN	α20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1658912 3' similar to contains Alu repetitive element;
8363	21056	34197	1.1	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8881	21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8881	21572	34716	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9122	21810	34976	4.3	9.0E-06	U36114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10858	23538	36784	3.46	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2532	15597	27888	1.27	8.0E-06	AW382539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
10430	23076	36288	0.75	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36289	0.75	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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958	13723		2.69	7.0E-06	AA689729.1	EST_HUMAN	ab00f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1419	14167	26851	3.42	7.0E-06	7682177	NT	MER20.11 MER20 repetitive element ; Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2876	15643		5.93	7.0E-06	AB688252.1	EST_HUMAN	qw16g09.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3551	16308		0.92	7.0E-06	AA385542.1	EST_HUMAN	EST89205 Thyroid Homo sapiens cDNA 5' and similar to EST containing L1 repeat
5509	18405		5.88	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0082-250400-173-h01 OT0082 Homo sapiens cDNA
5715	18508	31429	1.01	7.0E-06	N98845.1	EST_HUMAN	Y65e07.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278412 5'
8888	21380	34524	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
9800	22451		0.45	7.0E-06	Q61147	SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	25356	30508	2.32	7.0E-06	BF215972.1	EST_HUMAN	601881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2918	15684	28329	1.28	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0378-010300-105-d11 BT0378 Homo sapiens cDNA
3680	16433	28078	1.08	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0378-010300-105-d11 BT0378 Homo sapiens cDNA
4705	15708	28359	1.91	6.0E-06	Q01458	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4710	17442	30074	2.21	6.0E-06	A1040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ;
5265	18071	30700	1.32	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9766	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12755	25016	30978	2.27	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1i subunit (CACNA1I), mRNA
5970	18752	31713	3.27	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
6245	18019	31993	2.31	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7134	18921	32887	1.1	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8359	21052	34192	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8359	21062	34193	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10002	22650	35862	6.16	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10410	23056	36273	0.45	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12649	24953	30987	2.63	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	26048	6.1	4.0E-06	R16267.1	EST_HUMAN	ye48c03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
828	13596	26266	7.07	4.0E-06	AW103354.1	EST_HUMAN	xc65g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2689574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

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1311	14059	26733	4.84	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1311	14059	26734	4.84	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1457	14204	26889	1.8	4.0E-06	BF356612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2261	14988	27728	2.17	4.0E-06	AW015401.1	EST_HUMAN	U1-H-B10-aal-f-05-0-U.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3080	15928	28471	0.9	4.0E-06	AF198349.1	NT	<i>Gallus gallus</i> <i>Dach2</i> protein ( <i>Dach2</i> ) mRNA, complete cds
3874	16624	29262	1.05	4.0E-06	AW548295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4766	17488	30115	1.89	4.0E-06	A1868939.1	EST_HUMAN	w194c10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8397	21090	34225	0.56	4.0E-06	O16393	SWISSPROT	MER22 repetitive element ;
8999	21391	34536	3.56	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
8907	22260	35446	1.24	4.0E-06	AJ27285.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11427	23194	38425	4.21	4.0E-06	AB007855.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2160	14880	27824	1.75	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2160	14890	27825	1.75	3.0E-06	AA700562.1	EST_HUMAN	254b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element ;
2263	14889		1.44	3.0E-06	AF202635.1	NT	254b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element ;
2022	15688	28332	1.05	3.0E-06	AA866218.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3269	18021		2.05	3.0E-06	A1857779.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element ;
3763	18515	29152	1.13	3.0E-06	BE047094.1	EST_HUMAN	w122a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element ;
3763	18515	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74	3.0E-06	X54818.1	NT	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6068	18847	31811	0.93	3.0E-06	AU159412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
7129	19817		2.43	3.0E-06	P08548	SWISSPROT	AU159412 THYR01 Homo sapiens cDNA clone THYR01001602 3'
7981	20676	33801	0.83	3.0E-06	BE52994.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8584	21276	34413	0.68	3.0E-06	P07743	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 6'
12349	24755		3.84	3.0E-06	AW395282.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
197	13010		2.81	2.0E-06	P54366	SWISSPROT	RCO-LT0007-261189-011-A03 LT0007 Homo sapiens cDNA
1681	14308		4.45	2.0E-06	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
2376	15098	27838	4.8	2.0E-06	A1672138.1	EST_HUMAN	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
							w504a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1
							MER30 repetitive element ;

Page 200 of 536  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2463	15187	27928	2.37	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	16285	28023	1.68	2.0E-06	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16285	28918	1.12	2.0E-06	AA67555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFD805 3'
3744	16497	29132	1.58	2.0E-06	AA173518.1	EST_HUMAN	z02e05.11 Stragene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:695232 5'
3753	16505	28141	0.82	2.0E-06	AW450215.1	EST_HUMAN	UIH-B13-aky-g-05-0-UI.1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'
3758	16510	28148	1.82	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5998	18779		0.63	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1658609 3' similar to contains Alu repetitive element;
6028	18808	31788	0.63	2.0E-06	AI539448.1	EST_HUMAN	bt5105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080241 3' similar to TR:Q13537
6348	19118	32108	5.47	2.0E-06	AB19424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7818	20513		1.63	2.0E-06	AW869223.1	EST_HUMAN	W80604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410083 3'
7988	20683	33809	0.57	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0087-120400-002-102 SN0087 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H62051.1	EST_HUMAN	zh27c11.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9116	21804	34969	0.82	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9116	21804	34970	0.82	2.0E-06	AF003529.1	NT	y037c04.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9135	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9800	22253	35436	1	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9819	22470		0.63	2.0E-06	AV748989.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12251	25357	30609	2.1	2.0E-06	P23249	SWISSPROT	W16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
32	12860	25477	2.38	1.0E-06	O76082	SWISSPROT	yw66e03.s1 Soares_placenta_8to9weeks_2N8HP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
842	13421	26090	2.62	1.0E-06	AF084364.1	NT	AV748989 NPC Homo sapiens cDNA clone NPCAXD06 5'
1434	14181	26866	1.61	1.0E-06	P09125	SWISSPROT	PROTEIN MOV-10
1514	14261	26947	1.67	1.0E-06	AL163278.2	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1564	14311	26997	1.27	1.0E-06	AA034141.1	EST_HUMAN	Mus musculus D6M46E protein (D6M46E) mRNA, complete cds
1564	14311	26998	1.27	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
							z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
							contains Alu repetitive element;
							z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
							contains Alu repetitive element;
							DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1987	14723	27443	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1987	14723	27444	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4336	17075	29703	12.81	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5208	18016	30638	5.07	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-e06 BT0800 Homo sapiens cDNA
5232	18038	30665	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-080600-001-e04 FN0004 Homo sapiens cDNA
5232	18038	30668	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-080600-001-e04 FN0004 Homo sapiens cDNA
5389	18189	30881	1.22	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN/PRECURSOR
5708	18500		0.78	1.0E-06	BE083527.1	EST_HUMAN	CNO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
6773	19517	32545	8.91	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1-CHAIN PRECURSOR
7844	25427		0.83	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
7900	20595		0.77	1.0E-06	AA912823.1	EST_HUMAN	cl28c08.s1 Scores_NFL_T_GBC ST Homo sapiens cDNA IMAGE:1524878 3'
8171	20865	33997	1.2	1.0E-06	AI347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_Cc8 Homo sapiens cDNA IMAGE:1926842 3'
8387	21080	34215	1.31	1.0E-06	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA IMAGE:1982485 3' similar to contains element
9204	22083	35255	0.94	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element ;
9279	22033	35205	0.55	1.0E-06	Q39575	SWISSPROT	za55e01.e1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:286472 3'
9581	22234	35417	4.28	1.0E-06	U82688.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9581	22234	35418	4.28	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9627	22280	35470	4.76	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
9698	22340		3.37	1.0E-06	AA449257.1	EST_HUMAN	zo17e08.r1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
10385	23031		1.68	1.0E-06	AL163203.2	NT	zo04d1.1.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to
11648	24245		3.85	1.0E-06	AW880941.1	EST_HUMAN	gbD28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11724	24318	37641	1.38	1.0E-06	AA164914.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
11724	24318	37642	1.38	1.0E-06	AA164914.1	EST_HUMAN	RO4-NT0094-120500-012-b03 NT0054 Homo sapiens cDNA
12390	14723	27443	1.79	1.0E-06	AF184614.1	NT	zq42c02.s1 Stratiogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632354 3' similar to
12390	14723	27444	1.79	1.0E-06	AF184614.1	NT	SW;POL_SMSAV P03359 POL POLYPYRROLINE ;
351	13150	25790	2.24	9.0E-07	AF003529.1	NT	SW;POL_SMSAV P03359 POL POLYPYRROLINE ;
351	13150	25791	2.24	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
8308	21000		0.53	9.0E-07	AL163280.2	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
11212	23875	37161	2.87	9.0E-07	AL163281.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
							Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C081

Page 202 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24326	37650	1.3	9.0E-07	AF087813.1	NT	Human endogenous retrovirus HERV-P.1470
4719	17451	30084	3.26	8.0E-07	AI288998.1	EST_HUMAN	ql82g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4719	17451	30085	3.26	8.0E-07	AI288998.1	EST_HUMAN	ql82g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5796	18587		9.43	8.0E-07	P21414	SWISSPROT	POLYPROTEINCONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE
7901	20598		9.73	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		6.59	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Streptogene (cat#838206) Homo sapiens cDNA clone HFBEN89
11912	24476		8.22	8.0E-07	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	AF187341.1	NT	Homo sapiens membrane Interleukin 1 receptor accessory protein (IL-1RAP) gene, exons 10 and 11
5432	18231	30844	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30845	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	27352	2.98	6.0E-07	AW855558.1	EST_HUMAN	CM8-CT0277-221099-024-e11 CT02777 Homo sapiens cDNA
2488	16213	27958	4.52	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3955	18705		1.83	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF-P33 INTERGENIC REGION
9040	21730	34885	1.52	6.0E-07	BF001887.1	EST_HUMAN	7q94f07.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 O75920 4F5L.
11836	24420	37761	1.3	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12158	26307		2.28	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-260300-121-h12 NN1029 Homo sapiens cDNA
318	13121		1.94	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13785		4.25	5.0E-07	AA380630.1	EST_HUMAN	EST83619 Supt cells Homo sapiens cDNA 5' end
3028	15794		0.88	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6029	18809	31789	0.9	5.0E-07	U65087.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6964	19446	32463	1.69	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107963 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
6964	19446	32464	1.69	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107963 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7248	19933	33008	17	5.0E-07	AW070885.1	EST_HUMAN	xe31a02.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2688382 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33999	0.74	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8388	21081		0.82	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10285	22913	36123	4.94	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

Page 203 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23256	36493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11500	24101	37413	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.62	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12561	25211		3.48	5.0E-07	AW802537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3981	18729	28364	2.02	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7078	18769		0.83	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7187	18854	32923	1.74	4.0E-07	Q822V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7187	18854	32924	1.74	4.0E-07	Q822V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7823	20518	33644	0.6	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8949	21840	34787	5.41	4.0E-07	AW1419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2859548 3'
10027	22873	35890	0.47	4.0E-07	BE901975.1	EST_HUMAN	601878748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10027	22675	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601878748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10558	23536	38781	3.14	4.0E-07	AI765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
10856	23538	38782	3.14	4.0E-07	AI765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.66	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
431	13217	25862	9.64	3.0E-07	U19719.1	NT	Human microtubule-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
569	13350	25978	2.12	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1353	14101	28778	2.87	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1622	14369		2.03	3.0E-07	M64857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2039	14773		1.42	3.0E-07	AA528783.1	EST_HUMAN	nl56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element contains L1.13 L1 repetitive element ;
2286	15011	27749	1.83	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2472	15180	27930	7.81	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
2472	15180	27931	7.81	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
3031	15797	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	y450112.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:111696 6'
3167	15920	28568	1.45	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4711	17443	30075	0.86	3.0E-07	AI797236.1	EST_HUMAN	ws86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
5004	17727	30330	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5004	17727	30331	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

Page 204 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5580	18377	31280	12.43	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5883	18669	31610	0.83	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6603	18366		6.57	3.0E-07	AA815175.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7409	20088	33170	3.48	3.0E-07	AW787168.1	EST_HUMAN	cc04c10.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7561	20231		0.79	3.0E-07	AI691065.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA tw28f11.x1 NCI CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
9028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9028	21718	34873	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
11858	24253		1.75	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
12791	25043		5.1	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12855	25471	4.15	2.0E-07	AF282988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
150	12965	25606	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
150	12965	25607	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	12989	25629	44.15	2.0E-07	U38849.1	NT	Fugu tulipes beta-cytoplasmic (vascular) actin gene, complete cds
731	13505	28160	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	28161	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
922	13689	26353	3.73	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
923	13690	26364	2.15	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element;
1140	13885	26556	1.37	2.0E-07	Q28768	SWISSPROT	I66 AUTOANTIGEN
1596	14342	27032	2.98	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3676	19429	29070	15.93	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5059	17778	30395	0.84	2.0E-07	AW070896.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2667486 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS;

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5059	17778	30396	0.84	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
5260	18066	30394	1.21	2.0E-07	AW898066.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
6458	25090	32223	0.81	2.0E-07	AW449868.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6565	16830	32337	1.79	2.0E-07	AI208715.1	EST_HUMAN	UI-H-BIG-ake-b-01-0-UI.at1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
7568	20238	33342	0.67	2.0E-07	X96159.1	NT	q956405.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8369	21082		4.08	2.0E-07	AV728390.1	EST_HUMAN	H. sapiens brca2 gene exon 9
8695	21287	34426	0.97	2.0E-07	AA035198.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9661	22313		2.8	2.0E-07	AL163303.2	NT	z427g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10167	22815	38033	5.41	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10986	23032	38245	0.9	2.0E-07	P00751	SWISSPROT	CM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10988	23032	38246	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
11871	24945		2.44	2.0E-07	BE153717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11953	25212		2.39	2.0E-07	AI732482.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
1080	13838		1.97	1.0E-07	AL163282.2	NT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	PM0-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA
2830	14259	28045	2.51	1.0E-07	P09256	SWISSPROT	z185h11.x5 Stralagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:566028 3' similar to
3727	13638		1.29	1.0E-07	AL163282.2	NT	contains THR.b2 THR repetitive element ;
4260	17001	29631	2.76	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4260	17001	29632	2.76	1.0E-07	AV718662.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
4690	17424		0.93	1.0E-07	O75920	SWISSPROT	GLYCOPROTEIN GPV
5072	17791	30408	0.93	1.0E-07	AA019181.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
6410	19178	32177	0.87	1.0E-07	U82671.2	NT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6768	19512	32537	5.24	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	ZINC FINGER PROTEIN 189
7392	20071	33150	9.08	1.0E-07	N55081.1	EST_HUMAN	z556g02.l1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
7548	20218	33320	0.67	1.0E-07	BF375909.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cellactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LL>
7548	20218	33321	0.67	1.0E-07	BF375909.1	EST_HUMAN	z43406.y1 NC1 CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291339 5'
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	z43406.y1 NC1 CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291339 5'

Page 206 of 536

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385	33489	0.64	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33941	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33942	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691	2.78	1.0E-07	AA689576.1	EST_HUMAN	z157e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434348 3'
9170	21840	35005	0.87	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9517	22170	36353	0.45	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9836	22487	35689	2.77	1.0E-07	BF674524.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:4274428 5'
9844	22496	35696	1.21	1.0E-07	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
10362	23009		1.28	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12212	25188	30810	3.83	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:Q85722 O85722
12514	24864		1.87	1.0E-07	X61755.1	NT	DJ1163J1.1;
7181	19867	32940	0.84	9.0E-08	AI639662.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
9787	22438	35645	1.88	9.0E-08	AV734819.1	EST_HUMAN	ts51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090185 3'
11136	23804	37082	1.71	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cdABF806 5'
11668	24283	37567	2.8	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
12168	24648		4.44	9.0E-08	AI251973.1	NT	OFR repetitive element;
593	15546		3.7	8.0E-08	AI811352.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
1028	13788		0.72	8.0E-08	BE795469.1	EST_HUMAN	w16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3532	16286		1.53	8.0E-08	BE795469.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8638	21330	34474	3.05	8.0E-08	AI752367.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
6636	21330	34475	3.05	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9527	22180	35364	2.93	8.0E-08	AW970693.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
10461	23107	36336	0.47	8.0E-08	AF111167.2	NT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
11211	23874		2.1	8.0E-08	AF253417.1	NT	Homo sapiens [un dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
78	12904	25542	2.66	7.0E-08	Q02357	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1340	14088	26784	13.91	7.0E-08	X04809.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3563	16318	28965	1.15	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
							DYNEIN HEAVY CHAIN (DYHC)

Page 207 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28968	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 contarm Homo sapiens cDNA 3'
11672	24267	37589	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28966	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SOL gene locus
798	13570	26230	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
798	13570	26231	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0166-191199-004-g08 HT0166 Homo sapiens cDNA
3058	15924	28469	0.81	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	29588	0.98	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7851	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21806		0.56	6.0E-08	AA827075.1	EST_HUMAN	ab56c05.s1 NCL_CGAP_C0B1 Homo sapiens cDNA clone IMAGE:1336398 3' similar to contains MER12.b3 MER12 repetitive element;
11391	23997	37299	2.24	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11520	24120		1.33	6.0E-08	AL163209.2	NT	ENDONUCLEASE
83	12809	25547	3.72	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
2229	14957	27697	1.82	5.0E-08	AA493851.1	EST_HUMAN	hh03b09.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
11914	24477		8.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12089	24599	31086	2.54	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1754	14496	27195	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
1754	14496	27186	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
2888	15655		1.09	4.0E-08	AL078981.1	EST_HUMAN	DKFZp43J0428_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43J0428 5'
3894	16644	28284	1.04	4.0E-08	U82668.1	NT	Homo sapiens afox gene, alternatively spliced products, complete cds
6311	19082	32067	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8697	21389	34533	0.63	4.0E-08	O15993	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9037	21727	34881	1.05	4.0E-08	L42671.1	NT	Cricetus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9545	22198		0.71	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		0.68	4.0E-08	AI016342.1	EST_HUMAN	at78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10284	22932	36147	3.87	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;

Page 208 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11009	23881	36939	1.71	4.0E-08	AA393827.1	EST_HUMAN	z176b08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11009	23881	36940	1.71	4.0E-08	AA393827.1	EST_HUMAN	z176b08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11031	23702	36999	4.02	4.0E-08	BF692493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER. ;
11031	23702	36970	4.02	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
11919	25334		4.31	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
12549	24887		2.18	4.0E-08	AI34353.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
5523	18321	31222	2.22	3.0E-08	BE018348.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
5879	17955	30552	4.24	3.0E-08	AI792737.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
7439	20116	33205	1.98	3.0E-08	AL163246.2	NT	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
7649	20313		3.56	3.0E-08	AI436352.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
9798	22449		0.52	3.0E-08	AF095098.1	NT	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
10948	23626	36877	1.32	3.0E-08	AI218001.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
11566	24165	37477	61.58	3.0E-08	R86279.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
11566	24165	37478	61.58	3.0E-08	R86279.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
11888	24459		2.27	3.0E-08	R18420.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
201	13014		9.03	2.0E-08	AW302998.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
221	13033		9.14	2.0E-08	AA425598.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
484	13269	25905	1.01	2.0E-08	AF198349.1	NT	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
645	13424	26062	13.62	2.0E-08	AW886438.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
645	13424	26063	13.62	2.0E-08	AW886438.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
969	13735		24.4	2.0E-08	BE280477.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
1320	14069	26743	2.38	2.0E-08	AL163247.2	NT	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
1734	14476		12.18	2.0E-08	BE734871.1	EST_HUMAN	z165g03.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14885		4.11	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2845	15260		1.71	2.0E-08	K00216.1	NT	Sheep His-IRNA-GUG
3202	15865	28618	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15865	28619	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16391		1.76	2.0E-08	AW613620.1	EST_HUMAN	RC3-ST0197-161089-012-503 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.11 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
4903	17630		2.36	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2818327 3' similar to contains Alu repetitive element;
5549	18348	31265	1.19	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.e1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.93	2.0E-08	AV088924.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.B3 MER18 MER18 repetitive element;
7803	20598	33728	0.92	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8009	20704	33832	1.35	2.0E-08	AA490121.1	EST_HUMAN	ab02a08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3'
8983	21073		0.9	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23062	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	yw72i02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
10416	23062	36282	0.79	2.0E-08	N78097.1	EST_HUMAN	yw72i02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12184	24856		1.54	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1499	15571	26931	1.16	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1768	14510	27211	1.45	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2044	14777		2.31	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150699-001-f12 HT0130 Homo sapiens cDNA
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7688	20332	33443	1.26	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7934	20629	33756	0.52	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8028	20723	33855	0.64	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8028	20723	33856	0.64	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21137	34276	1.94	1.0E-08	AI015304.1	EST_HUMAN	o35a05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9104	21782		0.45	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9105	21783	34956	0.78	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA

Page 210 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8868	22516	35712	1.2	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10453	23099	36330	0.77	1.0E-08	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11285	23946	37241	4.14	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12282	24715		2.82	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4218	16959	29583	4.65	9.0E-09	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
4218	16959	29584	4.65	9.0E-09	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
8862	22610		0.52	9.0E-09	T97850.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121818 3'
6390	19159		0.62	8.0E-09	A1270615.1	EST_HUMAN	qu86a11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978984 3' similar to contains L1.13 L1 repetitive element;
7164	19851	32920	7.66	8.0E-09	A1183500.1	EST_HUMAN	q442a07.x1 Soares fetal heart NbhH10W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
7599	20594	33726	2.65	8.0E-09	AW600159.1	EST_HUMAN	CMO-NN1004-100300-273-608 NN1004 Homo sapiens cDNA
8887	21678		2.65	8.0E-09	AA938892.1	EST_HUMAN	op74a08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682575 3'
3593	16346		1.73	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7802	20497		0.61	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
7948	20841		0.82	7.0E-09	AA256200.1	EST_HUMAN	z80c06.r1 Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
8159	21829	34983	2.81	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10083	22731	35946	1.42	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10244	22892		0.5	7.0E-09	AA058626.1	EST_HUMAN	z68e07.s1 Soares retina N2b4IR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element;
10571	23268		1.49	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121818 3'
2149	14879		0.99	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
4922	17650	30263	3.12	6.0E-09	BE198421.1	EST_HUMAN	PM1-HT0927-160200-001-H05 HT0527 Homo sapiens cDNA
5298	18101	30760	11.59	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8476	21167	34311	0.93	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-H12 HT0446 Homo sapiens cDNA
9074	21763	34825	1.96	6.0E-09		NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10176	22824		3.76	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11798	24388	37722	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003702 Human adult (K.Okuho) Homo sapiens cDNA
1394	14141	26818	3.27	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1845	14583	27298	1.08	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6316	18087	32071	1.73	5.0E-09	AA369454.1	EST_HUMAN	EST68749 Fetal lung II Homo sapiens cDNA 5' end
6748	17917	30581	0.76	5.0E-09	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S913S>
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8995	22843	35855	2.22	5.0E-09	AW798667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
508	13292		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
944	13710		2.5	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1463	14200	26884	2.52	4.0E-09	9558718	NT	Homo sapiens chromosome 21 segment HS21C085
2016	14751	27478	2.31	4.0E-09	AF175325.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2016	14751	27480	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2430	15151	27885	6.07	4.0E-09	AA350878.1	EST_HUMAN	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
7746	20442	33565	0.59	4.0E-09	AA405747.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8420	21113	34250	0.82	4.0E-09	T64942.1	EST_HUMAN	zw04c06.r1 Scores_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:768288 5'
10779	23462	36704	2.06	4.0E-09	AL163209.2	NT	y411a07.s1 Scores fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:68804 3'
11011	23683	36943	1.47	4.0E-09	AI866401.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
11061	23731		1.53	4.0E-09	AA195142.1	EST_HUMAN	wm94f10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
2351	15073	27810	4.77	3.0E-09	BE222239.1	EST_HUMAN	z34a12.r1 Scores_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:885278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2557	15271	28008	1.2	3.0E-09	BE222238.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3
2658	16366	28104	1.13	3.0E-09	P23249	SWISSPROT	MER18 repetitive element;
3323	16083	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	PROTEIN MOV-10
3371	16130		1.08	3.0E-09	AA442272.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3
4076	16820		0.7	3.0E-09	X16674.1	NT	MER18 repetitive element;
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	z64a04.r1 Scores_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4478	17211	28836	1.65	3.0E-09	Q8Y3R6	SWISSPROT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
							Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
							258.1 KDA PROTEIN C21ORF5 (KIAA0933)

Page 212 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7800	20495	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCL_CGAP_K1411 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10147	22795	36009	1.7	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN.;
10945	23824	36873	4.8	3.0E-09	BF109943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10945	23824	36874	4.8	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
794	13568		2.43	2.0E-09	X16874.1	NT	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1235	13984	26653	7.99	2.0E-09	AL163284.2	NT	H sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1855	14401		7.46	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2326	15051	27787	1.1	2.0E-09	Q9Y3R5	SWISSPROT	DKFZp781B1710.1 t1 t61 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B1710 5'
3918	16868	28308	3.01	2.0E-09	O80241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (K1AA0933)
5076	17785	30411	0.85	2.0E-09	M23161.1	NT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5633	18428	31341	0.55	2.0E-09	A1004062.1	EST_HUMAN	Human transposon-like element mRNA
6058	18838		0.57	2.0E-09	AL163249.2	NT	ct47b09.s1 Soares_Testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6982	19599		0.93	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	EST169142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7423	20100	33188	0.68	2.0E-09	W28834.1	EST_HUMAN	z63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7717	20381	33494	0.82	2.0E-09	AW882126.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	MR1-CT0362-240200-105-408 CT0362 Homo sapiens cDNA
11233	23898	37183	1.62	2.0E-09	AL163248.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12428	13568		22.07	2.0E-09	X16874.1	NT	Homo sapiens chromosome 21 segment HS21C048
12495	26403		2.41	2.0E-09	AA226070.1	EST_HUMAN	H sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12834	24934		1.75	2.0E-09	U82868.1	NT	nc11c02.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
1087	13945	26503	2.01	1.0E-09	5031824	NT	z176d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	13845	26504	2.01	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17	1.0E-09	AJ228041.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2892	16659	28304	1.59	1.0E-09	U80017.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2928	15692	28336	3.25	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nalp) and survival motor neuron protein (smn) genes, complete cds
2928	15692	28337	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3034	16800	28446	0.7	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476		6.4	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5418	18215	30923	0.86	1.0E-09	AL163283.2	NT	Alu repetitive element; contains element MER22 repetitive element;
5740	18532	31455	1.89	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6053	18833	31795	3.13	1.0E-09	P26894	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8289	20983	34124	0.85	1.0E-09	AL688474.1	EST_HUMAN	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
10212	22860		2.92	1.0E-09	AL163283.2	NT	w439b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
11789	24389		1.88	1.0E-09	AL163283.2	NT	MER25.11 MER25 repetitive element;
12333	26344	30717	2.25	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
12503	24857		1.35	1.0E-09	T93176.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1286	14036	26707	3.74	9.0E-10	AW867740.1	EST_HUMAN	ye24e05.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118698 5'
2638	15606	28259	4.41	9.0E-10	AI870071.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
6735	19569	32801	4.76	9.0E-10	AI452982.1	EST_HUMAN	w678h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
142	12957	25599	13.27	8.0E-10	U63630.2	EST_HUMAN	SW-RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element PTR5 repetitive element;
3337	16097	28748	0.88	8.0E-10	BE080748.1	NT	948b09.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
4177	16917	28544	3.17	8.0E-10	AA376832.1	EST_HUMAN	TR:Q00372 Q00372 PUTATIVE P150.;
8865	22515		2.44	8.0E-10	U36308.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
685	13460	26707	9.36	7.0E-10	7706225	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
685	13460	26708	9.36	7.0E-10	Q13342	SWISSPROT	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
1618	14365	27055	2.24	7.0E-10	P08548	SWISSPROT	EST80564 Small intestine I Homo sapiens cDNA 5' end
2013	14748		3.17	7.0E-10	P08547	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2564	15278		24.23	7.0E-10	X00856.1	NT	Homo sapiens TPA Inducible protein (LOC51586), mRNA
3085	16850	28491	2.19	7.0E-10	AA345220.1	EST_HUMAN	Homo sapiens TPA Inducible protein (LOC51586), mRNA
6092	18870	31836	4.18	7.0E-10	BF352883.1	EST_HUMAN	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
7316	19699	33078	1.08	7.0E-10	P35084	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7556	20226		1.48	7.0E-10	AF029701.2	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7875	20570	33596	1.6	7.0E-10	AF029701.2	NT	H. sapiens DHFR gene, exon 3
7875	20570	33597	1.6	7.0E-10	AF029701.2	NT	EST51247 Gall bladder II Homo sapiens cDNA 5' end
10209	22857	36073	1.67	7.0E-10	L08895.1	NT	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
							DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
							Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens MADSMEF2-family transcription factor (MEF2C) mRNA, complete cds

Page 214 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
893	13662	26327	3.5	6.0E-10	AI400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2684	15393	28132	1.21	6.0E-10	AI424405.1	EST_HUMAN	h02407.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2095021 3'
4889	17423		2.7	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
8682	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
8882	21374	34519	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9534	22187	35373	0.46	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
11950	24503		2.16	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
745	13518		7.27	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
3468	16224	28878	2.5	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4931	17659	30269	1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7222	18907		1.51	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9436	22114	35288	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9436	22114	35289	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
109	12930		1.17	4.0E-10	AI221083.1	EST_HUMAN	qq09f09.x1 Soares_placenta_8to9weeks_2NbhP8a9W Homo sapiens cDNA clone IMAGE:1756049 3'
567	13348	25976	0.74	4.0E-10	AA516260.1	EST_HUMAN	similar to contains L1TR8.b2 L1TR8 repetitive element
1889	14725	27448	1.31	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
2580	15294	28032	3.73	4.0E-10	AL163303.2	NT	repetitive element
7076	19767	32831	25.71	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
10085	22743	35957	0.49	4.0E-10	AW283243.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10343	22980	36208	0.89	4.0E-10	AI267342.1	EST_HUMAN	UI-H-BI2-ah-a-07-0-U.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3'
895	13663	26329	3.55	3.0E-10	N36113.1	EST_HUMAN	ac83h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2039563
1329	14078		4.72	3.0E-10	AY005160.1	NT	ly32f06.s1 Soares_melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element
4498	17234	29864	1.04	3.0E-10	AL163203.2	NT	Homo sapiens extracellular glycoprotein lectin precursor, gene, complete cds
4498	17234	29865	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5368	18169	30855	1.24	3.0E-10	N50109.1	EST_HUMAN	yz11g08.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6110	18887	31856	2.52	3.0E-10	P20350	SWISSPROT	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6258	19032	32007	3.43	3.0E-10	BE302970.1	EST_HUMAN	bat6cd08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'

Page 215 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8629	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element:
8947	21638	34784	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
8947	21638	34785	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
9240	21919		0.58	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10359	23006		2.37	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
10493	23139		1.34	3.0E-10	AA769284.1	EST_HUMAN	nz38g03.s1 NCI CGAP GCBT1 Homo sapiens cDNA clone IMAGE:1289908 3'
12584	24907	31003	2.65	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
34	12882	25479	1.67	2.0E-10	P49988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12882	25480	1.67	2.0E-10	P49988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14627		1.96	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2986	15761		1.04	2.0E-10	BF676047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5714	18507		2.54	2.0E-10	Q28640	SWISSPROT	(HPRG)
6156	18933	31900	1.37	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A44) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	19963	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7912	20607	33737	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7912	20607	33738	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434565.1	EST_HUMAN	7o78d08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.18 L1 repetitive element:
11207	23958		1.37	2.0E-10	A1882153.1	EST_HUMAN	ta10f12.x1 Soares_tet1_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1498	14245		1.87	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-401 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AW652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2586	15300		3.16	1.0E-10	AW852001.1	EST_HUMAN	QVO-CT0226-161199-058-e08 CT0225 Homo sapiens cDNA
3481	16247	28901	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.7	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3996	16744		6.19	1.0E-10	AF13884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Page 216 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4108	16851	29477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	29478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4113	16856	29484	1.94	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	AI797745.1	EST_HUMAN	w82704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element ;
6720	19635	32678	0.86	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7376	20055		0.85	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7563	20261	33357	0.56	1.0E-10	AU128594.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138	20832	33968	1.04	1.0E-10	AW406990.1	EST_HUMAN	IB_044 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	AI269340.1	EST_HUMAN	qin04e10.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element ;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36754	2.65	1.0E-10	AI038280.1	EST_HUMAN	cy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11898	17913		1.71	1.0E-10	X87344.1	NT	H. sapiens DMA, OMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
255	13083	25702	1.59	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-281099-018-c08 HT0203 Homo sapiens cDNA
2097	14828	27661	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D2225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D2225 5'
2087	14828	27662	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D2225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D2225 5'
3378	16137	28795	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D2225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D2225 5'
3378	16137	28798	2.46	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D2225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D2225 5'
4465	17201	29827	1.03	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5487	18286		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-071-E08 BT0627 Homo sapiens cDNA
10054	22702	35919	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506808 5'
3114	15879		6.33	8.0E-11	H18971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element ;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3945	16695	29334	0.7	8.0E-11	AK78617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4022	16788	29398	4.88	8.0E-11	N23712.1	EST_HUMAN	yy46e08.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
6574	16338		0.85	8.0E-11	AW166158.1	EST_HUMAN	x45b11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1430	14177	26862	1.75	7.0E-11	AA330842.1	EST_HUMAN	MER10 repetitive element ;
							EST34392 Embryo, 8 week Homo sapiens cDNA 5' end
3852	16802	29240	1.03	7.0E-11	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8396	21089	34224	2.05	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22777		1.17	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
403	13188	25837	7.01	6.0E-11	M55270.1	NT	ENDONUCLEASE
403	13188	25838	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6822	19384	32398	0.67	6.0E-11	L44140.1	NT	Human matrix Gla protein (MGP) gene, complete cds
7593	20261	33369	3.65	6.0E-11	P08547	SWISSPROT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
8262	20956	34085	7.81	6.0E-11	AV727859.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9213	21892	35059	0.52	6.0E-11	BE063509.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCCASC08 5'
11	12838	25451	1.49	5.0E-11	AL163283.2	NT	CMD-BT0281-0311799-087-a03 BT0281 Homo sapiens cDNA
3359	12838	25461	1.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4203	16844	29571	1.36	5.0E-11	P48034	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
6423	18191	32187	1.63	5.0E-11	AL163213.2	NT	ALDEHYDE OXIDASE
7430	20107	33194	14.05	5.0E-11	11418799	NT	Homo sapiens chromosome 21 segment HS21C013
1380	14127		1.94	4.0E-11	AA436042.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH83), mRNA
2783	15498	28238	7.14	4.0E-11	BE885900.1	EST_HUMAN	zu01b12.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2869	15735	28385	1.16	4.0E-11	AL163247.2	NT	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
4578	17311	29939	0.85	4.0E-11	D44666.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6384	18153	32153	3.2	4.0E-11	P20095	SWISSPROT	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6903	19841	32886	0.82	4.0E-11	AA442630.1	EST_HUMAN	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7274	19958		4.5	4.0E-11	AF224669.1	NT	z469f10.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250
9295	21962		1.79	4.0E-11	BE149425.1	EST_HUMAN	G1055250 PHEROMONE RECEPTOR VN4. ;
9582	22215	35402	0.9	4.0E-11	AI609753.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
							RC1-HT0256-210100-013-008 HT0256 Homo sapiens cDNA
							tt2g12.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
							CE00385 ;

Page 218 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12462	24830	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1475	14222	26908	2.8	3.0E-11	6679077	NT	Mus musculus expressed in non-mesodermal cells 2, protein (NM23B) (Nm23), mRNA
4243	16884		1.04	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	AF150502.1	EST_HUMAN	q36c04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1162	13916	26580	3.99	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element ;
1162	13916	26581	3.99	2.0E-11	R24807.1	EST_HUMAN	Yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1608	14354	27042	4.86	2.0E-11	L17432.1	NT	Yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1608	14354	27043	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1612	14359	27048	1.21	2.0E-11	AF126374.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
3191	18954	28007	7.88	2.0E-11	P10263	SWISSPROT	qc51c10.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.1f L1' repetitive element ;
3320	16080	28730	1.11	2.0E-11	AK78617.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3356	16116	28771	0.93	2.0E-11	Q10473	SWISSPROT	tm64c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
3488	18244		1.01	2.0E-11	AF020503.1	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) [GALNAC-T1]
4409	17146		0.68	2.0E-11	BE065537.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4587	17302		0.72	2.0E-11	AL163227.2	NT	RC3-BT0318-170200-014-e05 BT0318 Homo sapiens cDNA
4882	17609		1.77	2.0E-11	BE062558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
6044	18824	31785	1.02	2.0E-11	AW877806.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
6218	18992	31968	1.87	2.0E-11	AA591028.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA
7095	18784	32850	0.59	2.0E-11	BF592945.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW.PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	7f97c03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3442565 3'
8123	21811		1.14	2.0E-11	AF028308.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
10184	22832	36046	5.44	2.0E-11	Q13606	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10413	23059	36277	1.12	2.0E-11	AW885874.1	EST_HUMAN	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10413	23059	36278	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
							RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA

Page 219 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726	36997	1.48	2.0E-11	AA035399.1	EST_HUMAN	zk27g02.e1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11058	23728	36998	1.48	2.0E-11	AA035399.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11090	23760	37035	1.57	2.0E-11	AA261958.1	EST_HUMAN	zs18b04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12017	26332		1.64	2.0E-11	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048	24567		3.54	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D26217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	26078	1.34	1.0E-11	AJ131018.1	NT	Homo sapiens SCL gene locus
1195	13947	26911	3.35	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1485	14232		2.36	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14765	27494	1.13	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
3490	16246	28900	1.2	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5249	18055	30683	16.93	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18533	31458	0.63	1.0E-11	BF222648.1	EST_HUMAN	7p57d01.x1 NCL_CGAP_PT28 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
8101	20795	33928	3.15	1.0E-11	4885546	NT	MER10 repetitive element ; Homo sapiens PHD finger protein 2 (PHF2) mRNA
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	y73d08.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
8948	21637	34782	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11267	23919	37212	1.62	1.0E-11	BF680078.1	EST_HUMAN	602164807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
9697	22348	35542	1.07	8.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9697	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9237	21916		0.93	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12125	24617		3.91	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4613	17348	29982	1.16	7.0E-12	Q05804	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11322	24013	37316	9.69	7.0E-12	AA704736.1	EST_HUMAN	z123g01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451162 3'
3535	16291		0.71	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
4314	17053	29678	8.52	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302673 3' similar to contains Alu repetitive element;
6295	19068	32051	0.77	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, cladenosine triphosphatase (FHT) gene, exon 5

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21585	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
8374	21949		1.87	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contig MIER29.12
1020	13780	28442	3.52	6.0E-12	T06673.1	EST_HUMAN	MER29 repetitive element ;
3385	16144	28801	1.61	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat#939206) Homo sapiens cDNA clone HFBVDV33
3713	18466	29104	5.03	5.0E-12	AJ271736.1	NT	h24b05.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291217 5'
5931	18715	31671	6.41	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5931	18715	31672	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	19168	32167	11.33	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6933	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
6942	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8128	20822	33959	1.33	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8566	21258		0.55	5.0E-12	AW687037.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8893	21584		0.54	5.0E-12	AL079581.1	EST_HUMAN	z101g12.s1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:376718 3' similar to contains
9006	21696	34847	2.93	5.0E-12	AJ271735.1	NT	L1.13 L1 repetitive element ;
9323	21990	35161	0.99	5.0E-12	P34982	SWISSPROT	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
10175	22823		4.45	5.0E-12	AL163303.2	NT	DKFZp434J0428_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0428 5'
10282	22910	36120	0.76	5.0E-12	AL163302.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10468	23114	36344	0.44	5.0E-12	6978754	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
237	13047	25686	4.2	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
238	13047	25688	4.03	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
4577	17312	28940	0.8	4.0E-12	AI689984.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
7619	20180		0.72	4.0E-12	BF445140.1	EST_HUMAN	z174g11.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
8141	20835		3.2	4.0E-12	AF109807.1	NT	b28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:460676 3'
8587	21276	34418	0.87	4.0E-12	AB042815.1	NT	MARINER TRANSPOSASE ;
11019	23691	36954	4.2	4.0E-12	AJ229043.1	NT	ned21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MIER7.b2
12375	24774		2.76	4.0E-12	U78027.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
							Bos taurus Mithc2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	28011	4.27	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SNRP.;
602	13380	28012	4.27	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SNRP.;
5084	17803	30421	0.81	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
5365	18167	30853	1.52	3.0E-12	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7654	20318		0.63	3.0E-12	AW854328.1	EST_HUMAN	RC3-C70255-031099-011-102 C70255 Homo sapiens cDNA
8273	20867	34109	0.51	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
8004	21994	34844	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10551	23247	36483	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10551	23247	36484	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1849	14395	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	IL6-JM0074-120400-065-a05 UM0071 Homo sapiens cDNA
4084	18338	29462	0.91	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4084	18338	29463	0.91	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4387	17124		2.03	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4840	17570	30192	1.18	2.0E-12	O70306	SWISSPROT	TX15 PROTEIN (T-BOX PROTEIN 15)
4840	17570	30193	1.18	2.0E-12	O70306	SWISSPROT	TX15 PROTEIN (T-BOX PROTEIN 15)
5169	17978	30491	0.77	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6385	19164		2.8	2.0E-12	AW871857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
7075	18768	32830	3.74	2.0E-12	T08169.1	EST_HUMAN	EST060660 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBBA13 5' end
7244	19929	33005	1.02	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-016-a08 HT0559 Homo sapiens cDNA
7558	20228	33331	2.2	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9208	22087		1.84	2.0E-12	AF196884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9885	22635		11.12	2.0E-12	BE166980.1	EST_HUMAN	MRS-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10412	23058	39278	0.87	2.0E-12	AL334130.1	EST_HUMAN	qq07602.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.;
12032	24557		2.81	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12223	24680		2.6	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SUL TX3), mRNA
119	12938	25578	2.21	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:28070040 3' similar to contains MER18.1 MER18 repetitive element;
1980	14716		1.39	1.0E-12	AI871728.1	EST_HUMAN	wn5107.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439483 3' similar to contains L1.b3 L1 repetitive element;
3067	15833	28476	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3087	16833	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	16805	29242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	16805	29243	28.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5877	18663		2.25	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5950	18732		1.93	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6438	19208	32202	0.62	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7016	18708	32784	2.07	1.0E-12	AF188864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7050	19741	32802	11.32	1.0E-12	AI248533.1	EST_HUMAN	q166a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:MI19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7050	19741	32803	11.32	1.0E-12	AI248533.1	EST_HUMAN	q166a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:MI19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8608	21288	34442	1.18	1.0E-12	AA782323.1	EST_HUMAN	ec26d05.s1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11273	23634		1.72	1.0E-12	AW468478.1	EST_HUMAN	he38f07.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2821317 3' similar to contains element LTR3 repetitive element;
11842	24497	37809	4.64	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGG ressequences, MAGG Homo sapiens cDNA
12150	24637		1.52	1.0E-12	AI738592.1	EST_HUMAN	w133h08.x1 NCI CGAP_Co18 Homo sapiens cDNA clone IMAGE:2392085 3'
12294	25308		2.92	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
3618	16371		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3927	16877	29320	0.98	9.0E-13	AB029900.1	NT	Homo sapiens GST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
8901	22154		2.67	8.0E-13	N89653.1	EST_HUMAN	za26b08.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:2636651 3'
700	13475	26123	7.37	8.0E-13	U29185.1	NT	Homo sapiens p10n protein (PrP) gene, complete cds
700	13475	26124	7.37	8.0E-13	U29185.1	NT	Homo sapiens p10n protein (PrP) gene, complete cds
1830	14569	27281	2.94	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nab) and survival motor neuron protein (smn) genes, complete cds
8011	20706	33834	0.78	8.0E-13	AI894398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437801 3'
8011	20706	33835	0.78	8.0E-13	AI894398.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437801 3'
10046	22894		3.08	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds

Page 223 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.67	8.0E-13	U66060.1	NT	Human germ-line T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
7718	20382	33495	0.71	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
7718	20382	33498	0.71	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8133	20827		0.56	7.0E-13	Q85165	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866813 5'
12617	24923		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAc-T1)
2084	14826	27558	6.75	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3318	16078		0.74	5.0E-13	R78338.1	EST_HUMAN	y8204.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3382	18151		1.54	5.0E-13	AA435773.1	EST_HUMAN	z77at12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
8777	19521	32548	0.84	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10787	23451	36593	2.72	5.0E-13	P07913	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1860	14598		2.23	4.0E-13	AW378814.1	EST_HUMAN	PM2-HT0224-221089-001-e11 HT0224 Homo sapiens cDNA
2462	16180		1.67	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5499	18297	31195	6.51	4.0E-13	BE189131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7105	19783	32858	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7512	20183	33277	0.94	4.0E-13	AA431528.1	EST_HUMAN	z778g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA.;
7620	20286		1.07	4.0E-13	N44291.1	EST_HUMAN	y93g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895 A32895 t complex sterility protein - mouse;
8740	21432	34577	1.07	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
9402	22084	35235	0.45	4.0E-13	AA076907.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
9919	22568	35764	4.94	4.0E-13	A1289831.1	EST_HUMAN	q932d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu repetitive element;
11120	23789	37068	2.09	4.0E-13	AA435819.1	EST_HUMAN	z778g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11120	23789	37067	2.09	4.0E-13	AA435819.1	EST_HUMAN	z778g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
175	12987		4.94	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
845	13616		1.62	3.0E-13	AA490310.1	EST_HUMAN	z768g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'

Page 224 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15092	27831	1.26	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
2483	15201		2.47	3.0E-13	AL103210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2669	15379	28117	2.91	3.0E-13	BF372962.1	EST_HUMAN	GM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3182	15945		2.97	3.0E-13	AA745844.1	EST_HUMAN	051802.51 NCI CGAP_K16 Homo sapiens cDNA clone IMAGE:1324035 3'
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:585315 5' similar to contains THR12 THR repetitive element;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:585315 5' similar to contains THR12 THR repetitive element;
5902	18687	31635	0.62	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:268890 3' similar to TR:O76139
7783	20478	33503	7.67	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), extendeukodystrophy protein >
7975	20670	33792	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
7975	20670	33793	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10098	22746	35961	0.72	3.0E-13	AW635487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10575	23270		3.81	3.0E-13	AI064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	36904	3.96	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11598	24197	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
145	12980	25802	3.42	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), extendeukodystrophy protein >
232	13043	25883	2.06	2.0E-13	U23838.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1247	13996	26663	7.99	2.0E-13	AF299710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	28419	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	28420	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	16036	28586	1.13	2.0E-13	BF431899.1	EST_HUMAN	hab7605.x1 Scarses_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3498	16254	28908	1.11	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4088	16931		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 225 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	18812	31772	4.7	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.58	2.0E-13	X78417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6747	19632	32675	7.15	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 8-phosphofructokinase (EC 2.7.1.11) exon 2
6954	19438	32451	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
6954	19438	32452	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	36219	3.87	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB2YL1) mRNA
12105	24602		3.48	2.0E-13	AW882155.1	EST_HUMAN	CMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
285	13091	25732	1.52	1.0E-13	S74128.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
888	13637	26307	5.64	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1313	14061	28738	1.08	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4553	17288	29917	1.64	1.0E-13	BF340887.1	EST_HUMAN	602038009F1 NCL_CGAP_Bin84 Homo sapiens cDNA clone IMAGE:4185868 5'
7810	20505	33628	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
7810	20505	33627	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
9990	22838		0.79	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10189	22847	36083	0.53	1.0E-13	AF300701.1	NT	Mus musculus osteostic protein tyrosine phosphatase mRNA, complete cds
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	745e10.x1 Scarses_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
11934	24492		2.25	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12563	24893		2.12	1.0E-13	AJ271735.1	NT	Homo sapiens Xa pseudautosomal region; segment 1/2
324	13125	25761	1.81	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Scarses_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
325	13128	25762	3.05	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Scarses_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
2504	15221		3.66	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-c09 CT0322 Homo sapiens cDNA
2599	15313	28050	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2599	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15483	28206	2.6	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3109	15874	28513	3.96	9.0E-14	AW513266.1	EST_HUMAN	xc64h05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707893 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3232	13126	25761	0.84	9.0E-14	AA781159.1	EST_HUMAN	ai24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
3778	16530	29169	0.85	9.0E-14	D14547.1	NT	repetitive element;
4707	17439	30071	1.66	9.0E-14	AJ002163.1	NT	Human DNA, SINE repetitive element
3489	16245		1.27	8.0E-14	BE468263.1	EST_HUMAN	Saginus oedipus gene for seminal vesicle secreted protein semenogelin I
3937	16887		2.67	8.0E-14	R76269.1	EST_HUMAN	h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
9348	20419	33539	15.04	8.0E-14	X89211.1	NT	W72603.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9460	22010	35180	3.69	8.0E-14	AA219316.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
11410	24059		1.72	8.0E-14	BE082558.1	EST_HUMAN	zq17c10.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:929970 3'
12302	24727	31056	2.48	8.0E-14	AI688118.1	EST_HUMAN	QV2-BT0268-261099-014-a01 BT0258 Homo sapiens cDNA
1625	15574		4.77	7.0E-14	AW151673.1	EST_HUMAN	wc92a08.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3'
8818	21510		10.57	7.0E-14	AL163285.2	NT	xi67e10.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
358	13158	25797	14.14	6.0E-14	AF020503.1	NT	MER10 repetitive element;
9722	22373	36572	2.6	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
9722	22373	35573	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
604	13382	26014	5.46	5.0E-14	Q63120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4893	17716	30322	1.41	5.0E-14	AW073781.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
6448	18245	31133	5.77	5.0E-14	P08547	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
1101	15560		2.18	4.0E-14	P04928	SWISSPROT	xc03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2675185 3' similar to contains L1.12 L1
1870	14608	27319	5.9	4.0E-14	AJ007973.1	NT	repetitive element;
3735	18488		0.87	4.0E-14	AA046502.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4259	17000	29630	1.05	4.0E-14	N46328.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
7858	20553		0.59	4.0E-14	X87344.1	NT	Homo sapiens LGMD2B gene
12626	25414		7.02	4.0E-14	AI889224.1	EST_HUMAN	zk07a06.t1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:487858 5'
930	13697	26361	1.88	3.0E-14	X95468.1	NT	W73c12.s1 Soares_multiple_sclerosis_2NbHNSP Homo sapiens cDNA clone IMAGE:278180 3' similar to contains L1.13 L1 repetitive element;
							H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
							wn08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435392 3' similar to contains Alu repetitive element;
							R.norvegicus mRNA for CPG2 protein

Page 227 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4870	17697	30220	0.92	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
4873	17600	30222	0.97	3.0E-14	7656884	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6835	19397	32411	1.49	3.0E-14	A1420788.1	EST_HUMAN	ts91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
6835	19397	32412	1.49	3.0E-14	A1420788.1	EST_HUMAN	ts91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
6744	25089		0.62	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8696	21378	34522	0.87	3.0E-14	N42165.1	EST_HUMAN	y07b10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270523 5'
10914	23594	36840	1.28	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 6'
11201	17597	30220	7.19	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
12539	25282		1.68	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
381	13168	25811	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
381	13168	25812	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
674	15548	26091	9.05	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2387	15108		1.49	2.0E-14	AW372888.1	EST_HUMAN	RG6-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2487	15185		2.15	2.0E-14		NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2529	15245	27983	1.19	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2542	15258		1.14	2.0E-14	BE222432.1	EST_HUMAN	h90g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element ;
2681	15390		0.95	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5437	18236	30950	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5533	18331	31236	0.92	2.0E-14	A812351.1	EST_HUMAN	ts78h01.x2 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.L3 L1 repetitive element ;
5834	18429	31342	3.42	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6794	19528		0.91	2.0E-14	BE000550.1	EST_HUMAN	RG3-BN0072-240200-011-e06 BN0072 Homo sapiens cDNA
6984	19877	32724	0.62	2.0E-14	4585709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7186	19871	32945	1.25	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7407	20084	33167	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7407	20084	33168	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
9817	22488	35671	0.57	2.0E-14	A1978795.1	EST_HUMAN	wr59g10.x1 NCL CGAP_UT1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10317	22884	36181	0.53	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBFBF04 5'

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10679	23370	36612	4.88	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B1-adv-a-10-Q-UI.c1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11691	24190	37507	1.29	2.0E-14	AW083959.1	EST_HUMAN	xc36102.x1 NCI CGAP_Co20 Homo sapiens cDNA clone IMAGE:2586363 3' similar to contains MIER1.13
12636	26284		2.29	2.0E-14	AF008191.1	NT	MER1 repetitive element;
1045	13804	26463	1.88	1.0E-14	AL163248.2	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
1385	14132	26805	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C046
1385	14132	26806	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1994	14730	27452	12.44	1.0E-14	L44140.1	NT	Homo sapiens chromosome 21 segment HS21C088
2182	14911	27843	4.55	1.0E-14	AL163303.2	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2409	15130	27866	3.56	1.0E-14	AF001689.1	NT	Homo sapiens chromosome 21 segment HS21C103
2945	15711	28363	1.79	1.0E-14	P08227	SWISSPROT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3165	15928	28576	5.42	1.0E-14	BF335227.1	EST_HUMAN	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3166	15928	28577	6.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3868	16816	29255	1.67	1.0E-14	AA882894.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
4440	17176	29802	1.91	1.0E-14	AW275852.1	EST_HUMAN	see89c12.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
5719	18511	31432	2.42	1.0E-14	AF126145.1	NT	xq39h10.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
6576	25095	32351	11.5	1.0E-14	11437150	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6576	25095	32352	11.5	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
11818	15928	28576	3.05	1.0E-14	BF335227.1	EST_HUMAN	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
11818	15928	28577	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
1570	14317	27002	2.06	9.0E-15	7427522	NT	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
2170	14899		1.43	9.0E-15	AF196779.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
7395	20074	33152	4.51	9.0E-15	P21416	SWISSPROT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$
7815	20670	33740	1.08	9.0E-15	BE903559.1	EST_HUMAN	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
12718	24991		2.36	9.0E-15	AL163247.2	NT	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
2814	13263		0.91	8.0E-15	BE261482.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
7081	18771	32836	1.14	7.0E-15	BF035327.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
10334	22981		3.07	7.0E-15	AW241958.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
973	13738	26403	8.64	6.0E-15	AJ271736.1	NT	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
						NT	Homo sapiens Xq pseudautosomal region; segment 2/2

Page 229 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	18618	31549	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
5829	18618	31550	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
401	13186	25834	6.63	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2764	15469	28212	1.38	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rchrt gene, and sodium phosphate transporter (NPT3) gene, complete cds
3481	16217		1.03	5.0E-15	AW298817.1	EST_HUMAN	UIH-BW0-ajb-g-10-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731218.3
10574	23269		2.4	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06.5
418	12829	25442	2.85	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6687	19332	32339	0.76	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10894	20392	33505	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10894	20392	33506	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4192	16933		7.06	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142.5 similar to ANFCARDIODILATIN
4872	17599		0.79	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
6716	18631		1.33	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7179	19865	32937	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7179	19865	32938	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9825	22476		2.51	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351784.3 similar to contains MER19.11
10694	23385	36625	2.47	3.0E-15	AB028688.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12310	25315		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12814	25056		1.35	3.0E-15	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-a01 P.T0034 Homo sapiens cDNA
243	13052	25692	3.6	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25799	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28810	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28811	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Page 230 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4049	16794	28423	1.08	2.0E-15	AW238489.1	EST_HUMAN	xp28101.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741621 3' similar to contains L1.13 L1 repetitive element;
4690	17315		2.46	2.0E-15	AI806335.1	EST_HUMAN	w07006.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2349823 3' similar to TR:Q61043 Q61043 NINEIN.;
6089	18887	31833	0.88	2.0E-15	BE662352.1	EST_HUMAN	601344263F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677288 5'
6089	18887	31834	0.88	2.0E-15	BE662352.1	EST_HUMAN	601344263F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677288 5'
7014	19706		1.5	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7171	19857	32828	2.62	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7294	19977	33054	5.18	2.0E-15	W05064.1	EST_HUMAN	z178d10.11 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
8804	21496	34642	2.86	2.0E-15	D14547.1	NT	WP:F44F4.8 CE02227 TRANSPOSASE.;
8971	21681	34811	1	2.0E-15	AA397768.1	EST_HUMAN	Human DNA, SINE repetitive element
8971	21681	34812	1	2.0E-15	AA397768.1	EST_HUMAN	z177g08.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35145	1.23	2.0E-15	AW378465.1	EST_HUMAN	z177g08.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35146	1.23	2.0E-15	AW378466.1	EST_HUMAN	CMO-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
10742	23428		5.66	2.0E-15	AJ271795.1	NT	CMO-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
12451	25338		2.04	2.0E-15	U82828.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12653	16256	28910	3.34	2.0E-15	AF223391.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12653	16256	28911	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2777	15482		2.39	1.0E-15	AI689984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3011	15777	28427	1.35	1.0E-15	BE043584.1	EST_HUMAN	b28105.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
3139	15903	28548	1.29	1.0E-15	P08547	SWISSPROT	h140e02.y1 NCL CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5'
5138	17866		0.97	1.0E-15	AW021431.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6279	19052	32030	1.74	1.0E-15	T95763.1	EST_HUMAN	d123e06.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2484202 5'
6909	19847		2.12	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MERG repetitive element;
8131	20825	33961	0.86	1.0E-15	AL163280.2	NT	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
8319	21012	34149	4.56	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8319	21012	34160	4.56	1.0E-15	AI200976.1	EST_HUMAN	q68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21628	34770	0.67	1.0E-15	AL163207.2	NT	q68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

Page 231 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8940	21631	34774	1.78	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9148	21877	35042	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9632	22185	35370	0.94	1.0E-15	AA864653.1	EST_HUMAN	ch37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
10720	23409	36651	3.6	1.0E-15	AF04083.1	NT	repetitive element;
12722	25148	30896	4.72	1.0E-15	AI763944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4469	17204	29830	0.98	9.0E-16	4503168	NT	element;
10915	23595	36841	2.04	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (COAT displacement protein) (CUTL1) mRNA
11696	24291	37615	1.46	9.0E-16	A1244341.1	EST_HUMAN	HSC23F081 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11698	24291	37616	1.46	9.0E-16	A1244341.1	EST_HUMAN	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
5615	18411	31324	0.71	7.0E-16	4885120	NT	MER10 repetitive element;
7241	18928	33001	1.49	7.0E-16	O88807	SWISSPROT	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7241	19928	33002	1.49	7.0E-16	O88807	SWISSPROT	MER10 repetitive element;
12675	25237		1.98	7.0E-16	T94149.1	EST_HUMAN	Homo sapiens chemokine (G-C motif) receptor 8 (CCR8) mRNA
2137	14867		8.38	6.0E-18	AW972811.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
1476	14223	26909	1.08	5.0E-16	AJ251154.1	NT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
2687	16396	28134	2.17	5.0E-16	AA992176.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
9954	22802	35806	0.54	5.0E-16	AL163246.2	NT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
11504	24105	37418	3.6	5.0E-16	BF217368.1	EST_HUMAN	ye28c12.11 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:119062 5'
12757	26018		14.19	5.0E-16	11418127	NT	EST384702 MAGC resequences, MAGL Homo sapiens cDNA
2233	14981		1.81	4.0E-16	AB001523.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2378	15100	27839	1.77	4.0E-16	AW797168.1	EST_HUMAN	ol80c04.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
2378	15100	27840	1.77	4.0E-16	AW797168.1	EST_HUMAN	contains element L1 repetitive element;
3450	16206	28856	3.58	4.0E-16	Q16663	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
4121	16863	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4121	16863	29490	5.02	4.0E-16	BE083875.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
7612	20278	33386	46.62	4.0E-16	AL163284.2	NT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
							QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
							MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084

Page 232 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8105	21865	35029	1.04	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133	1.91	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
11851	24435	37778	1.44	4.0E-16	Q62632	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24547		2.04	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24609	31087	2.91	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (GAB2), mRNA
130	12945	25589	2.03	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	12945	25590	2.03	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
453	13239		1.5	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
483	13248		1.5	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	14182	26887	1.38	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2975	15741	28388	3.76	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3913	16663	29304	19.63	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
3939	16689		0.85	3.0E-16	U03887.1	NT	Human BXP20 gene
5186	18004		0.99	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5529	18327	31230	1.79	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8556	21248	34387	4.26	3.0E-16	AI002836.1	EST_HUMAN	em98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR.b2 THR repetitive element;
9780	22441		0.89	3.0E-16	BF690617.1	EST_HUMAN	602248538F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4332032 5'
10019	22667	35683	5.57	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
951	13717		1.2	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2385	15105		0.91	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares testis NIH-Homo sapiens cDNA clone IMAGE:1030855 3'
2694	15403		1.08	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4157	16897	29526	1.16	2.0E-16	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
4447	17183	29807	0.96	2.0E-16	AI208733.1	EST_HUMAN	qg56f03.x1 Soares testis NIH-Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
5104	17822	30439	0.79	2.0E-16	BE061178.1	EST_HUMAN	MER29 repetitive element;
6642	19404	32419	0.99	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA
7615	20281	33389	0.75	2.0E-16	AI470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
7867	20562	33689	2.14	2.0E-16	AI732837.1	EST_HUMAN	tf16e11.x1 NCI CGAP_Gaas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
8058	20762	33883	0.57	2.0E-16	BE658026.1	EST_HUMAN	MER33 repetitive element;
							nz47f06.x5 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849
							HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905; contains MER7.11 MERY repetitive element;
							7182109.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'

Page 233 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8038	20752	33884	0.57	2.0E-16	BE58026.1	EST_HUMAN	7182h09.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8425	21118	34257	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
180	12992	25630	1.84	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13198		29.68	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Sceres_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1893	14699	27414	2.37	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5635	18430	31343	0.75	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6341	19111		27.85	1.0E-16	U45993.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6479	19246	32246	3.39	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7453	19111		7.15	1.0E-16	U45993.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9183	21853	35019	1.07	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3722	16475	29112	2.11	8.0E-17	AW800048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6624	19386		2.2	9.0E-17	AI392984.1	EST_HUMAN	ig22e11.x1 NCI CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element;
8007	20702		4.76	9.0E-17	AW160257.1	EST_HUMAN	xg49g12.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2830850 3' similar to contains OFR.12 OFR repetitive element;
10124	22772		2.47	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
997	13757		1.77	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA
3872	16622		0.87	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5486	25069	31193	3.7	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0569-060300-003-e04 HT0569 Homo sapiens cDNA
7175	19891		1.94	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1441	14188		3.44	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5240	18046		3.3	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6588	19351	32365	8.05	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cytoskeletal transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
198	13011	25653	8	6.0E-17	AW983980.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6221	18995	31971	1.64	6.0E-17	AW662772.1	EST_HUMAN	h181d04.x1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element;
10190	22838	36053	0.46	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
412	12823	28436	2.97	5.0E-17	T84110.1	EST_HUMAN	yc05h08.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7486	20158	33250	2.09	5.0E-17	T81043.1	EST_HUMAN	yd26b04.r1 Sceres fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:108327 5'

Page 234 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3828	16379	28020	0.69	4.0E-17	AA643697.1	EST_HUMAN	n196605.61 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
9282	22016	35184	1.07	4.0E-17	AW129185.1	EST_HUMAN	x120e04.x1 NCI_CGAP_K148 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11475	24076	37386	2.64	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12027	24555		1.75	4.0E-17	A1073546.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840288 3' similar to TRQ16530
1477	14224		1.14	3.0E-17	D14547.1	NT	Q16530 PMS3 MRNA ; contains MER10.12 MER10 repetitive element ;
2091	14822	27554	1.85	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3188	15951		1.18	3.0E-17	P38410	SWISSPROT	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3633	16388	29026	1.34	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633	16386	29027	1.34	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
4970	17695		1.89	3.0E-17	BF511266.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
8166	20860	33992	5.16	3.0E-17	N69451.1	EST_HUMAN	UI-H-B14-a01-c08-Q-U1.1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
9601	22254	35439	6.58	3.0E-17	AB026898.1	NT	zai14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element ;
10278	22927	36140	0.64	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10279	22927	36141	0.64	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11994	24532		3.65	3.0E-17	11417866	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12784	26023		1.44	3.0E-17	AV720204.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
343	13144	25782	3	2.0E-17	A1270080.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCIDF08 5'
344	13144	25782	2.17	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
987	13733		1.84	2.0E-17	AA722932.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2448	15167	27904	2.21	2.0E-17	Q28983	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2448	15167	27905	2.21	2.0E-17	Q28983	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2930	15696	28343	6.64	2.0E-17	P12038	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
5282	18087	30745	1.88	2.0E-17	M27685.1	NT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
5282	18087	30746	1.88	2.0E-17	M27685.1	NT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
6171	18948		2.04	2.0E-17	AF050068.1	NT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
6388	19167		1.16	2.0E-17	AL134881.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
7882	20677	33802	1.12	2.0E-17	Q95156	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;

Page 235 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8366	21049	34188	1	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9769	22420	35028	2.81	2.0E-17	BE289888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860616 5'
9804	22455	35657	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804	22455	35658	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10159	22807	36025	4.82	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	22926	36138	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	22926	36139	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10307	22954	36169	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348718 3'
10307	22954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348718 3'
733	13507	26164	3.66	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446		1.26	1.0E-17	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1761	14503	27204	2.73	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2109	14840	27571	2.35	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2335	15069	27785	2.06	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	16309		1.3	1.0E-17	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4119	16858		7.37	1.0E-17	R03942.1	EST_HUMAN	(UBE2D3) genes, complete cds
6366	19136		0.69	1.0E-17	AW488468.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:128388 5'
6555	19320	32327	2.04	1.0E-17	A185642.1	EST_HUMAN	repetitive element; contains LTR8.1 LTR8 repetitive element;
6555	19320	32328	2.04	1.0E-17	A185642.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6889	19882	32730	0.93	1.0E-17	Q16831	SWISSPROT	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
8490	21182	34324	1.33	1.0E-17	BE062744.1	EST_HUMAN	URIDINE PHOSPHORYLASE (UDRPASE)
8907	22556	35751	0.88	1.0E-17	AW996538.1	EST_HUMAN	QV0-BT0263-101289-072-d07 BT0263 Homo sapiens cDNA
11394	24000	37304	2.09	1.0E-17	Q28824	SWISSPROT	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11732	24325	37649	2.47	1.0E-17	AA453647.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2474	15192	27632	0.95	9.0E-18	AA174078.1	EST_HUMAN	G1263081 MARINER TRANSPOSASE. ;
8388	22060		3.31	9.0E-18	A1472187.1	EST_HUMAN	zp189712.s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609862 3'
3766	16518	28158	1.52	8.0E-18		NT	ij86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
					4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
339	13140	25776	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

Page 236 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7343	20024	33100	1.33	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA
12492	13140	25776	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12492	13140	25777	3.41	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3289	18050	28698	1	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
4698	17432		3.02	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8148	20842		2.84	6.0E-18	11428165	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC634448), mRNA
8248	20840	34077	0.72	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11079	23749	37024	1.61	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
11300	23660	37280	1.74	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12241	24692	31076	3.29	6.0E-18	U87929.1	NT	Human acetylcholinesterase (AChE) gene, exon 4
1125	13881	26541	21.7	5.0E-18	AI280214.1	EST_HUMAN	qnr65g11.x1 Soares_placenta_86weeks_2NHP869W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
5047	17768	30384	0.98	6.0E-18	D61517.1	EST_HUMAN	HUM411F08B Clontech human fetal brain polyA+ mRNA (#6635) Homo sapiens cDNA clone GEN-411F08 5'
5191	17959	30622	1.2	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8620	21312	34454	6.25	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
10899	23579	36828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10899	23579	36828	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12368	24770		3.4	5.0E-18	AW867182.1	EST_HUMAN	MFR1-SN0035-080400-001-g11 SN0035 Homo sapiens cDNA
12895	24978		4.18	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
121	12939	25580	1.37	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29 b3 MER29 repetitive element;
121	12939	25581	1.37	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29 b3 MER29 repetitive element;
1711	14454	27153	1.18	4.0E-18	AAG21814.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29 b3 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	14819		1.12	4.0E-18	AI738592.1	EST_HUMAN	wf33h08.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'

Page 237 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2199	14927	27662	1.33	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2199	14927	27663	1.33	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3772	16524	29162	0.68	4.0E-18	A1581586.1	EST_HUMAN	ar93606.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5279	18084	30740	2.24	4.0E-18	A1017565.1	EST_HUMAN	cu23e06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5279	18084	30741	2.24	4.0E-18	A1017565.1	EST_HUMAN	cu23e06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7745	20441		0.63	4.0E-18	AA746811.1	EST_HUMAN	rx64a08.s1 NCL_CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.L2.L1 repetitive element;
10927	23607	36859	8.76	4.0E-18	AA371807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
828	13599	26270	1.68	3.0E-18	AA814196.1	EST_HUMAN	cb23h11.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5;
909	13078	26340	3.47	3.0E-18	BE088634.1	EST_HUMAN	CNM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
3931	16631	29322	1.47	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6730	16584	32596	5.64	3.0E-18	BE001671.1	EST_HUMAN	PM0-BN0081-700300-001-508 BN0081 Homo sapiens cDNA
10844	23526	36769	1.61	3.0E-18	BF218650.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
12497	24852		6.14	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
244	13053	26593	4.42	2.0E-18	AW636920.1	EST_HUMAN	QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA
1130	13886		62.93	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5326	18129		3.19	2.0E-18	AA868810.1	EST_HUMAN	ak53a07.s1 Scores_testis_NH-T Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5419	18218	30927	3.68	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5419	18218	30928	3.68	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5788	18579		1.68	2.0E-18	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Bm07 Homo sapiens cDNA clone IMAGE:4156670 5'
6073	18852	31817	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6073	18852	31818	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6185	18962	31935	1.04	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6226	19000	31977	5.18	2.0E-18	AW665853.1	EST_HUMAN	h94g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879984 3' similar to contains MER19.12 MER19 repetitive element;
7336	20018	33096	0.81	2.0E-18	AA457619.1	EST_HUMAN	aa89d11.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77;
8047	20741	33873	0.47	2.0E-18	BE439524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9947	22595	35798	1.66	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
9947	22595	35799	1.66	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
10894	23574	36824	2	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876499 3' similar to contains THR.b3 THR repetitive element;
11736	24329	37653	3.91	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
12174	13886		1.45	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4382	17119		1.02	1.0E-18	T95409.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
5271	18077	30707	3.63	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'
5483	18282	31180	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5483	18282	31181	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6363	19193	32128	1.53	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8341	21034	34171	1.43	1.0E-18	AI148288.1	EST_HUMAN	oz69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.11 L1 repetitive element;
9799	22450	36653	4.22	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12130	24621	31082	4.23	1.0E-18	AF003529.1	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
532	13316	25952	5.34	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
533	13316	25952	3.24	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7747	20443		4.47	9.0E-19	F08698.1	EST_HUMAN	MER19 repetitive element;
9598	21280	34419	2.54	9.0E-19	AL163203.2	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8598	21280	34420	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11072	23742	37016	4.82	9.0E-19	AB032969.1	NT	Homo sapiens chromosome 21 segment HS21C003
11901	13316	25952	1.88	9.0E-19	AA281961.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
1026	13786		1.25	8.0E-19	AW974902.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
4372	17110		1.04	8.0E-19	P08548	SWISSPROT	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8048	20742	33874	0.92	8.0E-19	BE158936.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA

Page 239 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4758139	NT	Homo sapiens DEAD/HD (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX8) mRNA
6384	19134	32129	2.34	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7199	19885	32959	0.9	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
9911	22580	35758	0.51	7.0E-19	A1344951.1	EST_HUMAN	h01c08.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3'
12036	25397		2.05	7.0E-19	AA705684.1	EST_HUMAN	z60b01.s1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3761	16513		1.34	6.0E-19	AW852930.1	EST_HUMAN	PMO-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4430	17109	29795	1.38	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4430	17109	29796	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4747	17479		1.3	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4987	17692	30301	1.04	6.0E-19	AL120817.1	EST_HUMAN	DKFZp782F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782F192 5'
5787	18558	31485	5.36	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
10324	22971	36191	1.03	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11525	24125	37431	7.45	5.0E-19	AW183725.1	EST_HUMAN	x87b02.x1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2884171 3' similar to contains element MSR1 repetitive element;
541	13324	28956	1.68	4.0E-19	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2699	15398	28136	1.02	4.0E-19	BF097362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5311	18115	30773	0.97	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3833	16594	29219	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3833	16594	29220	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4263	16994	29622	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4263	16994	29623	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413	17160	29777	1.12	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5198	18006		0.64	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7283	18966		2.79	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
9359	20430	33548	1.15	3.0E-19	X89885.1	NT	M.musculus mRNA for TPCR33 protein
12284	24709		23.34	3.0E-19	AF165620.1	NT	Homo sapiens parvalbumin 1 (protein (PBI)) mRNA, complete cds
2565	15279	28017	21.33	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4411	17148		1.03	2.0E-19	A1311783.1	EST_HUMAN	q991e02.x1 NCI CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1916898 3' similar to TR:Q69386 Q69386 POL/ENV GENE;
5963	18745	31706	0.57	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'

Page 240 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7238	18923	32898	0.93	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20922	34061	8.08	2.0E-19	AA012854.1	EST_HUMAN	z834c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9809	22480	35666	0.68	2.0E-19	Q85156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11829	24413	37760	1.33	2.0E-19	BF330887.1	EST_HUMAN	RC3-BT0333-250800-114-704 BT0333 Homo sapiens cDNA
11829	24413	37761	1.33	2.0E-19	BF330887.1	EST_HUMAN	RC3-BT0333-250800-114-704 BT0333 Homo sapiens cDNA
469	13255		1.87	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2161	14891	27626	1.58	1.0E-19	H30795.1	EST_HUMAN	y678g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2723	15430		2.37	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2851	15819		4.95	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3398	16154	28806	1.2	1.0E-19	AA834967.1	EST_HUMAN	ej49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5983	18764	31728	2.38	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6114	25419		0.83	1.0E-19	AA585627.1	EST_HUMAN	rh22d03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:983093 similar to contains L1.11 L1 repetitive element;
7528	20199	33293	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7528	20199	33294	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7695	25118		0.93	1.0E-19	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8348	21042	34179	1.75	1.0E-19	M54657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8640	21332		2.64	1.0E-19	T99920.1	EST_HUMAN	y672b02.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
9849	22301		0.46	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10087	22735	35950	23.03	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191098-031-b05 ST0174 Homo sapiens cDNA
10097	22745	35950	1.46	1.0E-19	N44631.1	EST_HUMAN	yj31e09.r1 Soares melanocytes 2NfHM Homo sapiens cDNA clone IMAGE:272872 5'
11780	24351	37683	1.55	1.0E-19	U83183.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
6549	19314	32319	2.58	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6549	19314	32320	2.58	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7418	20095	33180	1.34	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7418	20095	33181	1.34	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3270	16031	28692	1.41	7.0E-20	BF329456.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
6898	17872	30529	6.29	7.0E-20	AL139120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547D092 5'
8394	21097	34222	12.48	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.b2

Page 241 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
11714	24308		1.95	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3543	16298	28948	3.52	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4239	16980	28605	3.33	6.0E-20	BE822434.1	EST_HUMAN	601441231F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3916231 5'
4568	17291		1.18	5.0E-20	AV725123.1	EST_HUMAN	AV728123 HTC Homo sapiens cDNA clone HTc8TA01 5'
7015	19707	32763	1.07	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HAO250
7848	20541	33688	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
7848	20541	33689	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8002	20697	33625	0.7	5.0E-20	BE165980.1	EST_HUMAN	MR3-H70487-150200-113-g01 HT0487 Homo sapiens cDNA
8734	21426	34572	2.54	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8734	21426	34573	2.54	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9345	20416		0.94	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1618	14363	27054	1.34	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5562	18359		0.8	4.0E-20	Q98980	SWISSPROT	HISTONE H2B C (H2B(C))
7826	20521		5.15	4.0E-20	AI874352.1	EST_HUMAN	tb84g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:22893386 3'
10368	23042	38259	1.33	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2135	14865	27595	1.02	3.0E-20	U03888.1	NT	Human BXP21 gene
4185	18926	28557	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4582	17317	28944	1.05	3.0E-20	AA037616.1	EST_HUMAN	z436b12.s1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
8833	21525		2.95	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10219	22867	36078	0.93	3.0E-20	BF185264.1	EST_HUMAN	601843581F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
10561	23257		1.87	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11486	24097	37408	1.5	3.0E-20	AI284244.1	EST_HUMAN	qj70d02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11486	24097	37409	1.5	3.0E-20	AI284244.1	EST_HUMAN	qj70d02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12051	24569	31118	2.66	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
811	13582		3.12	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2767098 3' similar to SW:RS6_MOUSE P87461 40S RIBOSOMAL PROTEIN S6.;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	AA516335.1	EST_HUMAN	ng68h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.
1089	13847	26506	3.37	2.0E-20	AA516335.1	EST_HUMAN	ng68h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.
2820	13582		2.38	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS6_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.
4893	17620	30238	4.97	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4893	17620	30239	4.97	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5067	17786		5.98	2.0E-20	5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8017	20712	33843	0.81	2.0E-20	AA309457.1	EST_HUMAN	EST180326 Liver III Homo sapiens cDNA 5' end
9089	21778	34942	8.6	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9089	21778	34943	8.6	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12426	25141	30885	2.03	2.0E-20	H56371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
12815	25057		1.39	2.0E-20	11437152	NT	Homo sapiens heparin-binding growth factor binding protein (HBP17), mRNA
2007	15525	27468	3.71	1.0E-20	AA281981.1	EST_HUMAN	z11406.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
4406	17143	29772	1	1.0E-20	BF115158.1	EST_HUMAN	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element;
6794	19538	32566	0.75	1.0E-20	AF049567.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
9061	21750	34909	2.04	1.0E-20	11418491	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11541	24141	37450	2.62	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12171	24651		1.73	1.0E-20	AA420453.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1 repetitive element;
2913	15879		0.98	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library/Homo sapiens cDNA clone MPIp112-8J21
11804	24669		2.62	9.0E-21	AW898189.1	EST_HUMAN	RC3-NN0068-080500-021-b03 NN0068 Homo sapiens cDNA
8711	21403		2.15	8.0E-21	AW674891.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN O85169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR;
11526	24126	37432	3.52	8.0E-21	AA809411.1	EST_HUMAN	cb71f06.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1336835 3'
12084	24679		4.49	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2061	14793	27518	1.62	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2061	14793	27519	1.62	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3688	16442	28083	0.69	7.0E-21	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4228	16989		5.58	7.0E-21	AA048502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'

Page 243 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6340	19110	32100	0.79	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287	20981	34121	1.53	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8576	21268	34407	10.76	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10013	22681	38877	0.86	7.0E-21	AW86822.1	EST_HUMAN	RCO-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
10594	23288	36525	2.19	7.0E-21	AA723404.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.13 OFR repetitive element ;
11234	23897	37184	1.75	7.0E-21	7706668	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4083	16827	28454	0.83	6.0E-21	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9034	21724	26334	0.6	6.0E-21	BE162737.1	EST_HUMAN	PM1-HIT0454-080100-002-h09 HIT0454 Homo sapiens cDNA
903	13670	26334	0.7	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330	17069	26697	2.91	5.0E-21	BE668830.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3633880 5'
4749	17481	30112	5.58	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6655	18582		0.8	5.0E-21	AW440864.1	EST_HUMAN	he05e10.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
6917	18654	32700	0.86	5.0E-21	BE866505.1	EST_HUMAN	7183d11.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1 OFR repetitive element ;
10474	23120	36349	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10474	23120	36350	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11986	24527		2.83	5.0E-21	AA393574.1	EST_HUMAN	z172c04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1727	14469	27168	1.81	4.0E-21	AA970713.1	EST_HUMAN	co86e08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573034 3' similar to TR:Q16530 Q16530 PMS3 MRNA, contains OFR.t1 OFR repetitive element ;
6772	18516	32544	3.27	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9680	22332	35527	0.63	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9705	22356	35552	0.7	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1829	14588	27280	0.84	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stratagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:628771 3'
2272	14998	27736	1.24	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3078	15843	28485	4.31	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5412	18211	30919	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30920	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5

Page 244 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5682	18447		0.65	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLGGOA10 3'
6086	18864		2.3	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
6969	19451	32468	7.69	3.0E-21	BF381083.1	EST_HUMAN	RG1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9592	22245	35428	1.15	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12533	25327	30714	2.88	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
141	12856		17.18	2.0E-21	BE163247.1	EST_HUMAN	GV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
914	13681	26342	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
914	13681	26343	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944		2.75	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h06 BT0311 Homo sapiens cDNA
2844	15354	28098	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2844	15354	28098	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5386	18198	30890	1.64	2.0E-21	A1624582.1	EST_HUMAN	ts30f03.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5488	18288	31184	0.68	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5489	18288	31185	0.68	2.0E-21	AA027211.1	EST_HUMAN	ze97a12.1 Scores_fetal heart_NbrH19W Homo sapiens cDNA clone IMAGE:366910 5'
8170	20864	33996	0.5	2.0E-21	AJ010770.1	NT	ze97a12.1 Scores_fetal heart_NbrH19W Homo sapiens cDNA clone IMAGE:366910 5'
8281	20955	34094	6.16	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
8722	21414	34557	3.74	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
10891	23665		1.55	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11289	23950	37246	1.3	2.0E-21	BE973829.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.b3
11289	23950	37247	1.3	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element ;
12272	24712		9.87	2.0E-21	AF178815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3851008 5'
1233	13982	26652	1.6	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3851008 5'
1381	14128		2.62	1.0E-21	A1601264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
6396	18185		2.74	1.0E-21	AL079752.1	EST_HUMAN	nt46c04.e1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
7092	19781	32847	6.6	1.0E-21	AI223104.1	EST_HUMAN	MER29 repetitive element ;
10484	23130		1.07	1.0E-21	5730038	NT	ar88d12.x1 Bardeford colon HPLR77 Homo sapiens cDNA clone IMAGE:2162343 3'
4377	17114	29747	6.65	9.0E-22	A1702438.1	EST_HUMAN	DKFZp43410830_j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp43410830 5'
8502	21194	34336	1.27	9.0E-22	AL163201.2	NT	qg47e05.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:U64241 QM
8502	21194	34337	1.27	9.0E-22	AL163201.2	NT	PROTEIN (HUMAN) ;
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							ts94a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT ;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001

Page 245 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10891	23382	36622	2.63	8.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
11707	24302	37627	1.34	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLAGE2000394 5'
929	13898		5.55	8.0E-22	BE144748.1	EST_HUMAN	CM0-H107179-281099-076-h08 HT0179 Homo sapiens cDNA
7767	20492		3.72	8.0E-22	AA046302.1	EST_HUMAN	Zk67a06.1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
650	13428	26087	5.92	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4250	16991	29816	2.21	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4977	17700	30307	0.99	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8590	21282		1.38	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8731	21423	34568	3.56	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Strategene (cath936208) Homo sapiens cDNA clone HFBCF07
9502	22155	35335	2.04	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4038	16793	29413	0.98	8.0E-22	AA405040.1	EST_HUMAN	zu65d10.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:742887 5'
8140	20834		1.33	8.0E-22	AW026123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2642812 3'
6424	19192	32188	3.78	8.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10217	22865	36077	7.83	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12499	24854		2.22	5.0E-22	BF476811.1	EST_HUMAN	naa27b08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3627	16380		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8004	20699	33827	0.45	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8312	25428		3.11	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10623	23316	36558	2.47	4.0E-22	BF218030.1	EST_HUMAN	G01882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12657	24957		2.06	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
939	13708		1.58	3.0E-22	A1469879.1	EST_HUMAN	ttn14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element;
2576	15289	28028	0.92	3.0E-22	A1859038.1	EST_HUMAN	w166b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW_RL21_HUMAN P49778 60S RIBOSOMAL PROTEIN L21.;
3682	16415		1.48	3.0E-22	D14718.1	NT	Human chromosomal protein HMGI related gene
4748	17480	30111	2.6	3.0E-22	A1090126.1	EST_HUMAN	qb28c07.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697560 3' similar to contains MER1212 MER12 repetitive element;
8129	20823		0.8	3.0E-22	BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA
8134	20828	33963	2.46	3.0E-22	BE089841.1	EST_HUMAN	RCS-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8288	20952	34088	0.97	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8258	20952	34089	0.97	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1946	14681		2.29	2.0E-22	N24942.1	EST_HUMAN	yk73d05.st Scores_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:267369 3'
2528	15242	27981	2.15	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3414	16172	28821	4.41	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4200	16941	29597	1.17	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0282-281199-001-d12 ST0282 Homo sapiens cDNA
5761	25075	31476	1.18	2.0E-22	W39458.1	EST_HUMAN	zc2001.1 Soares_senescent_fibroblasts_NbHSP Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6084	18862	31828	3.68	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0078-150800-025-h12 TN0078 Homo sapiens cDNA
9602	22255	35440	1.53	2.0E-22	A1276522.1	EST_HUMAN	q176h08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878298 3' similar to contains
9898	22347	35540	0.89	2.0E-22	AA715315.1	EST_HUMAN	MER29.i3 MER29 repetitive element;
9898	22347	35540	0.89	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
11781	24352	37984	1.68	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
11872	24946	30983	3.74	2.0E-22	AL163280.2	NT	h22404.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2874655 3'
1871	14609	27320	1.79	1.0E-22	AW885517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2588	16302	28038	1.1	1.0E-22	U50871.1	NT	PM4-SN0020-010400-008-h02 SN0020 Homo sapiens cDNA
3405	16163	28814	1.37	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7641	20308	33415	0.89	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10451	23097	36328	0.79	1.0E-22	A1365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
10451	23097	36329	0.79	1.0E-22	A1365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2020881 3' similar to contains MER29.b2
12704	24984	28959	5.89	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3557	16312	28959	0.79	8.0E-23	AF198349.1	NT	IL2-JM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3306	16065	36895	2.55	7.0E-23	AV647248.1	EST_HUMAN	Galus gallus Dach2 protein (Dach2) mRNA, complete cds
10868	23842	36895	4.16	7.0E-23	5031952	NT	AV647248 GLC Homo sapiens cDNA clone GLCAW007 3'
3427	18194	28601	1.72	6.0E-23	AF198333.1	NT	Homo sapiens Nct56 (D. melanogaster)-like protein (NOT66L) mRNA
4235	16976	28601	1.39	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12005	24540	31105	1.5	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
12005	24540	31106	1.5	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12182	24663	31087	3.28	6.0E-23	A1209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5358	18160	30844	4.09	6.0E-23	U82871.2	NT	qg59c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>

Page 247 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6145	25086	31893	3.93	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7337	25086	31893	3.37	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6347	19117	32108	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6347	19117	32107	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7738	20434	33556	4.1	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element ;
9148	21879	35045	2.98	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9148	21879	35046	2.98	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10215	22863		1.18	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0068-270400-011-h01 NN0068 Homo sapiens cDNA
651	13428	26068	4.25	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1120	15520		3.87	2.0E-23	M53270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2798	15503	28243	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2798	15503	28244	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3394	16123		1.46	2.0E-23	A1201458.1	EST_HUMAN	qs73f11.x1 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:1943767 3' similar to TR:Q13537 Q13537
3705	16458		3.35	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3958	16707	28346	3.66	2.0E-23	H59931.1	EST_HUMAN	MR3-HIT0487-150200-113-g01 HIT0487 Homo sapiens cDNA
3958	16707	28347	3.65	2.0E-23	H59931.1	EST_HUMAN	yr16a02.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							yr16a02.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7772	20468		4.3	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
8742	21434	34579	1.21	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
11991	24530		2.45	2.0E-23	M32658.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12508	24860		2.87	2.0E-23	AF009660.1	NT	Homo sapiens chromosome 21 segment HS21C052
4482	17228	29857	1.1	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
4714	17446		5.56	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6820	18382		3.28	1.0E-23	BE378471.1	EST_HUMAN	601230455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
							zw82c08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTRS.12 PTRS repetitive element ;
8254	20948	34085	4.6	1.0E-23	AA448097.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
10570	23265	36503	2.05	1.0E-23	BE408643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
10570	23265	36504	2.05	1.0E-23	BE408643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
							ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852768 3' similar to TR:E19822 E19822 CA PROTEIN ;
539	13322		1.84	9.0E-24	AA663213.1	EST_HUMAN	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
6397	18127	32121	1.63	8.0E-24	11422027	NT	

Page 248 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3853	16603		1.49	7.0E-24	AW637954.1	EST_HUMAN	QVQ-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
5087	17808		0.95	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
10536	23233		1.33	7.0E-24	AW303317.1	EST_HUMAN	xx1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
690	13465		2.72	6.0E-24	AB001421.1	NT	Macaca fascicularis mRNA for Testis-Specific Protein Y (TSPY), complete cds
818	13589	26256	11.74	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3953	18703	29342	7.9	6.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7657	20321	33430	0.58	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11595	24194	37513	1.45	5.0E-24	AW514229.1	EST_HUMAN	hd24b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910413 3' similar to TR:O94851 O94851 KIAA0750 PROTEIN. ;
5840	18628	31563	3.85	4.0E-24	AA584178.1	EST_HUMAN	nm31105.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW_POL_MLVVK P31795 POL POLYPROTEIN ;
8581	21273	34411	1.35	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-006 ST0197 Homo sapiens cDNA
11133	23801	37078	1.95	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484498 5'
12381	24765	31082	4.89	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12595	24951	30996	1.77	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8322	21016		2.85	3.0E-24	AW614871.1	EST_HUMAN	hh88c08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987950 3' similar to contains MER29.b2 MER29 repetitive element ;
8377	21070		1.57	3.0E-24	AW962076.1	EST_HUMAN	EST374149 IMAGE: resequences, MAGG Homo sapiens cDNA
9365	21840	35114	4.33	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12438	24808	31045	1.41	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053398 5'
2346	15069	27806	2.72	2.0E-24	AA167539.1	EST_HUMAN	zp1109.r1 Stratagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:609161 5'
3778	16531		1.01	2.0E-24	AW698189.1	EST_HUMAN	RC3-NN0088-090500-021-503 NN0088 Homo sapiens cDNA
7374	20054	33135	0.81	2.0E-24	AF088824.1	NT	Mus musculus rho/rac-interacting citron kinase (Cikl) mRNA, complete cds
7379	20059	33138	0.65	2.0E-24	AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-6H13
8639	21331	34476	3.28	2.0E-24	AL119158.1	EST_HUMAN	DKFZp781L1712_r1 781 (synonym: harny2) Homo sapiens cDNA clone DKFZp781L1712 5'
8878	21368		0.98	2.0E-24	H69214.1	EST_HUMAN	yr82b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
9754	22405	35611	0.94	2.0E-24	AI521759.1	EST_HUMAN	tf77a09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
9754	22405	35612	0.94	2.0E-24	AI521759.1	EST_HUMAN	tf77a09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
11825	24408	37744	1.31	2.0E-24	AW868552.1	EST_HUMAN	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA
11825	24409	37745	1.31	2.0E-24	AW868552.1	EST_HUMAN	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA
12281	25377		7.44	2.0E-24	M28877.1	NT	Human O family dispersed repeat element

Page 249 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1691	14435	27131	2.69	1.0E-24	7708340	NT	Homo sapiens CGI-127 protein (LOC51849), mRNA
2679	15398		1.63	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3020	16786	28433	1.49	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4237	16978		1.71	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7447	20123	33214	4.32	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7630	20296	33404	0.81	1.0E-24	BE144528.1	EST_HUMAN	MR0-HT0168-271199-005-d09 HT0168 Homo sapiens cDNA
7845	20540	33667	2.09	1.0E-24	AW901164.1	EST_HUMAN	CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
11899	24294	37819	1.31	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
4939	17687	30275	2.33	7.0E-25	AA483944.1	EST_HUMAN	ne02e10.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:911764 similar to contains MER1.b2 MER1 repetitive element;
8117	20811	33946	6.59	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
11701	24296	37622	3.28	7.0E-25	AA583540.1	EST_HUMAN	nt25h06.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
6893	17989		4.9	6.0E-25	W87623.1	EST_HUMAN	P38105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
7622	20288	33397	8.34	8.0E-25	7305360	NT	zh65h07.r1 Scores fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
1647	14393	27093	1.18	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus obogelin (Obog), mRNA
11286	23947	37242	2.44	5.0E-25	AW979107.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
1429	14176	26861	2.26	4.0E-25	T98107.1	EST_HUMAN	EST391217 IMAGE sequences, MAGP Homo sapiens cDNA
3397	16155		3.04	4.0E-25	AW887671.1	EST_HUMAN	ye66h04.r1 Scores fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:121783 5'
4282	17021		2.93	4.0E-25	BE170957.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
3314	16074	28724	3.98	3.0E-25	8923321	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3314	16074	28725	3.98	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4837	17568	30190	0.75	3.0E-25	P28622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6518	19284	32298	0.6	3.0E-25	AA603590.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8235	20929	34085	4.86	3.0E-25	AL163210.2	NT	np27b02.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M81868 ZINC FINGER PROTEIN 85 (HUMAN);
10959	23635	36886	1.89	3.0E-25	AA679013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1328	14075	28749	2.94	2.0E-25	5032186	NT	repetitive element;
2306	15031	27768	6.42	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2835	15259	27897	3.67	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4167	16907	29535	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4167	16907	29536	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16

Page 250 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9665	22317	35514	1.94	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Starvies GS) Homo sapiens cDNA
355	13163	25784	1.03	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1226	13976		2.02	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2435	16166	27890	1.03	1.0E-25	Q08055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 6) (SUBUNIT C)
4806	17637	30160	2.84	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
6472	18239		0.79	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stralagene hNT neuron (#337233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
6089	25100	32657	3.14	1.0E-25	AA582890.1	EST_HUMAN	nm54h11.s1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1087749 3'
7814	20509	33633	4.03	1.0E-25	AA709079.1	EST_HUMAN	z86g04.s1 Soares_fetal_heart_Nbx-H19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element;
9446	22123	35302	0.75	1.0E-25	X60860.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
9446	22123	35303	0.75	1.0E-25	X60860.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
10890	23570	36821	3.06	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12768	25024		2.18	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2487	15204	27845	1.41	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
5607	18403		1.99	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1571	14318	27003	1.72	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3982	16711	28351	1.23	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4139	16890	29509	2.27	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808366 3'
5551	18348	31257	0.62	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11689	24284		8.45	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stralagene neuroepithelium NT2RAMJ 837234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gbM14339 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12547	24885		1.64	7.0E-26	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGE Homo sapiens cDNA
2222	14850	27689	2.04	8.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3341	16100	28752	0.95	6.0E-26	AA208131.1	EST_HUMAN	zq52h04.r1 Stralagene neuroepithelium (#337231) Homo sapiens cDNA clone IMAGE:645271 5'
10432	23078	36301	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10432	23078	36302	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11683	24278	37600	2.03	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1154	13909	26572	3.61	6.0E-26	AI708236.1	EST_HUMAN	es38h08.x1 Barstled aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318519 3' similar to WP.F49C12.11 CE03371;

Page 251 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1154	13909	28573	3.61	5.0E-26	AI08235.1	EST_HUMAN	as38h08.x1 Berstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2310519 3' similar to WP:F49C12.11 CE03371;
1535	14282		1.4	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
9312	21979		3.72	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10558	23284	36491	2.75	4.0E-26	BE268187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1753	14495	27184	1.21	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1896	14732	27464	1.31	3.0E-26	AL045955.2	EST_HUMAN	DKFZp4341066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341066 5'
2025	14760		3.15	3.0E-26	AA115895.1	EST_HUMAN	z30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	16512	29148	1.04	3.0E-26	AA152464.1	EST_HUMAN	z30f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3760	16512	29148	1.04	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
6811	19472	32485	1.78	3.0E-26	BF245458.1	EST_HUMAN	z30f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
10828	23319		1.42	3.0E-26	AF036405.1	NT	G695374 THYROID RECEPTOR INTERACTOR;
11559	24158	37468	1.83	3.0E-26	AW875651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
11559	24158	37468	1.83	3.0E-26	AW875651.1	EST_HUMAN	60186493F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11602	24201	37523	6.56	3.0E-26	AA583173.1	EST_HUMAN	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11858	24442	37783	1.38	3.0E-26	AF228925.1	NT	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
12724	24995		2.52	3.0E-26	AW073434.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
686	13442	26083	6.76	2.0E-26	AL163282.2	NT	m37d05.s1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
1861	14598		3.07	2.0E-26	AL038099.2	EST_HUMAN	OFR repetitive element;
3226	16988	28842	5.89	2.0E-26	X86894.1	NT	Mus musculus harmonin isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
5147	17866		1.09	2.0E-26	AF073482.1	NT	xa57b09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2670873 3' similar to contains MER30.11
10653	23344		2.7	2.0E-26	D87675.1	NT	Mus musculus chromosome 21 segment HS21C082
11180	23846	37132	3	2.0E-26	AI801412.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
11386	24001		2.45	2.0E-26	AF055066.1	NT	DKFZp566L171_s1 566 (synonym: hfk42) Homo sapiens cDNA clone DKFZp566L171 3'
12106	24603		1.57	2.0E-26	AB037859.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-16
133	12948	25591	5.18	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens myotubularin related protein 7 mRNA, partial cds
2040	14774	27503	1.37	1.0E-26	AL038099.2	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
2693	15402		9.04	1.0E-26	AF261085.1	NT	to89a01.x1 NCL_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element;
							Homo sapiens MHC class I region
							Homo sapiens mRNA for KIAA1438 protein, partial cds
							QV4-HT05938-020300-123-e02 HT05938 Homo sapiens cDNA
							DKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

Page 252 of 536  
Table 4  
Single Exon Probes Expressed in Brain

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6740	19574		3.05	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10809	23492		2.21	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
12348	26395		3.53	1.0E-28	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 6'
7484	20156		1.11	9.0E-27	BF371227.1	EST_HUMAN	RC8-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9203	22082		4.14	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11875	24454		5.72	9.0E-27	BF445558.1	EST_HUMAN	naa03c07.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:3253044 3' similar to contains OFR.t1 OFR repetitive element ;
10	12837	25450	3.83	8.0E-27	AI831492.1	EST_HUMAN	wj48cd4.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element ;
544	13327		4.33	8.0E-27	AL163221.2	NT	Homo sapiens chromosome 21 segment HS21C027
1395	14142	26819	59.39	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1395	14142	26820	59.39	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2164	14893	27628	1.37	8.0E-27	AW854776.1	EST_HUMAN	PM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
3180	15943	28594	1.81	8.0E-27	P12238	SWISSPROT	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
3348	16107	28762	0.81	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5608	18404	31317	1.02	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBC808 6'
6861	17957		2.53	8.0E-27	BE926560.1	EST_HUMAN	MR4-BT0398-250800-204-408 BT0398 Homo sapiens cDNA
6947	19429	32444	2.29	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
9109	21797	34951	1.51	8.0E-27	AW857579.1	EST_HUMAN	REPETITIVE ELEMENT L1
9109	21797	34952	1.51	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA
668	13444		1.23	7.0E-27	Z70864.1	NT	CM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA
5030	17750		2.25	7.0E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element HC2
8756	21448		1.19	7.0E-27	D66984.1	NT	h151h12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:076040
10950	23341		4.26	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
12484	24843		2.12	7.0E-27	AV723365.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
10527	23320	36558	2.76	6.0E-27	M26597.1	NT	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
11804	24394	37728	1.57	6.0E-27	U93163.1	NT	Human nuclear protein (B23) mRNA, complete cds
							Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

Page 253 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10137	22785	35996	2.82	5.0E-27	BF66614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10137	22785	35997	2.82	5.0E-27	BF66614.1	EST_HUMAN	602121491F1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:4278527 5'
6845	19407	32421	1.65	4.0E-27	8910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7840	20535		1.07	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7883	20578		1.54	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9844	22266	35491	0.7	4.0E-27	AW880859.1	EST_HUMAN	QV0-O70033-070300-152.b10 OT0033 Homo sapiens cDNA
11604	24203	37525	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2034	14789	27499	4.61	3.0E-27	X80858.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4238	16978	29604	1.06	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-080100-001-d11 BT0527 Homo sapiens cDNA
5282	18069	30697	6.24	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7688	20381	33475	0.63	3.0E-27	BE870351.1	EST_HUMAN	7c3302.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9205	22084	35256	2.93	3.0E-27	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'
40	12888	25487	14.84	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1888	14625		5.12	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3107	15872		10.39	2.0E-27	AW629172.1	EST_HUMAN	hi51h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875679 3' similar to TR:O76040
3218	15991	28632	1.98	2.0E-27	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3218	15981	28633	1.86	2.0E-27	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4009	16765	28385	1.38	2.0E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6577	19340	32353	0.61	2.0E-27	H02655.1	EST_HUMAN	y36a01.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
7989	20894	33810	1.65	2.0E-27	A1865347.1	EST_HUMAN	SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;
9169	21839		2.3	2.0E-27	AA551527.1	EST_HUMAN	w28g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9691	22342	35536	0.76	2.0E-27	X80658.1	NT	nh08h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
9935	22593	35782	1.28	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
9935	22593	35783	1.28	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
10875	23555	36802	4.11	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
11489	14625		3.31	2.0E-27	AA565345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
426	13212		1.51	1.0E-27	AL163246.2	NT	nk01b10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C046

Page 254 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
976	13741	28404	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4061	16806		0.98	1.0E-27	BE360127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element ;
6449	19217	32215	6.26	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6771	19515	32542	1.96	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
6771	19515	32543	1.98	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8508	21200	34346	0.98	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8894	21575		2.26	1.0E-27	BE079780.1	EST_HUMAN	RC8-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
9822	22275	35463	2.55	1.0E-27	D87449.1	NT	Human mRNA for KIAA0280 gene, partial cds
11704	24288	37625	3.51	1.0E-27	AF111083.1	NT	Bos taurus latrophilin 3 splice variant brain mRNA, complete cds
137	12951		2.94	9.0E-28	BE348399.1	EST_HUMAN	hwt7c11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
303	13107	25747	3.31	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
10289	22837	36150	0.63	9.0E-28	AA174078.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443.6'
11051	24504		4.85	9.0E-28	BF377859.1	EST_HUMAN	zp18g12.s1 Striatogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:608662 3'
12286	25245		2.46	8.0E-28	AW157571.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1158	13913	26576	7.89	7.0E-28	AU142750.1	EST_HUMAN	eu83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0565 PROTEIN, contains element MER22 repetitive element ;
11442	23809	37089	3.36	7.0E-28	11417868	NT	AU142750 Y78AA1 Homo sapiens cDNA clone Y78AA1000824 5'
11810	24474		2.78	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
8817	21509		0.97	6.0E-28	AF016052.1	NT	AV735348 CB Homo sapiens cDNA clone CBFAXA12 5'
12526	24873		2.35	6.0E-28	AA504582.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF181 (ZNF181) gene, complete cds
310	13114		4.19	5.0E-28	AI921003.1	EST_HUMAN	aa80e03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR6 repetitive element ;
3990	16738	28372	1.44	6.0E-28	R79762.1	EST_HUMAN	wo18c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
2631	15343	28087	1.68	4.0E-28	AW185086.1	EST_HUMAN	y89f10.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:146443 5'
2878	15742	28389	0.78	4.0E-28	4505316	NT	xn33c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
3106	15871	28511	2.62	4.0E-28	BE409100.1	EST_HUMAN	Q08379 GOLGIN-95 ;
7230	18915	32988	1.93	4.0E-28	AI108941.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA G01300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5' qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

Page 255 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10774	23457		3.08	4.0E-28	AF028308.1	NT	Homo sapiens chromosome 8 duplication of the T cell receptor beta locus and tyrosinase gene families
10828	23608		17.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10850	18915	32988	4.75	4.0E-28	A189841.1	EST_HUMAN	qf68f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12312	24734		1.84	4.0E-28	AW894244.1	EST_HUMAN	RC3-CT0254-240-400-210-112 CT0254 Homo sapiens cDNA
1280	14009		2.88	3.0E-28	AF165382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5051	17770		1.05	3.0E-28	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8728	21418	34562	1.89	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-409 HT0713 Homo sapiens cDNA
10853	23633	36778	2.09	3.0E-28	U53688.1	NT	Homo sapiens MHC class 1 region
12344	24751		3.62	3.0E-28	A1831801.1	EST_HUMAN	wj98707.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element :
87	12913	26551	10.6	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1023	13783	26444	0.86	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1142	13897	26558	16.03	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
2481	15199	27839	2.1	2.0E-28	A1348634.1	EST_HUMAN	qo35b06.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.B2 L1 repetitive element :
8215	18989	31968	1.33	2.0E-28	BF224402.1	EST_HUMAN	h176c03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element :
8238	19012		5.07	2.0E-28	BF212905.1	EST_HUMAN	601814186F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048761 6'
7843	20838	33765	0.71	2.0E-28	AF005273.1	NT	Sus scrofa domestica submandibular epimucrin mRNA, complete cds
9484	22137		5.54	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
11614	24212	37538	1.84	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12322	24741		2.22	2.0E-28	H06376.1	EST_HUMAN	Y79c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 6'
1461	14208	26895	2.84	1.0E-28	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2217	14945	27685	2.37	1.0E-28	BF333238.1	EST_HUMAN	QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA
7759	20455		3.2	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC630391), mRNA
7917	20612		3.3	1.0E-28	8022793	NT	Homo sapiens hypothetical protein FLJ10958 (FLJ10958), mRNA
9178	21848	35014	4.84	1.0E-28	AA308744.1	EST_HUMAN	EST179815 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
9776	22427	35633	8.73	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9776	22427	35634	8.73	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA

Page 256 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10422	23068		0.63	1.0E-28	AU149356.1	EST_HUMAN	AU149356 NT2RM4 Homo sapiens cDNA clone NT2RM4002146 3'
11916	24478		7.79	1.0E-28	AA094182.1	EST_HUMAN	z51c01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
12651	25143		1.88	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12749	25346	30603	3.18	9.0E-29	AW663987.1	EST_HUMAN	h176g06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12436	24806		3.32	8.0E-28	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1598	14344	27034	1.37	7.0E-28	AW966447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
12794	26046		7.13	7.0E-28	AJ132352.1	NT	Rattus norvegicus mRNA for 46 kDa secretory protein, partial
581	13361	25989	16.66	6.0E-28	AJ936748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12201	24669		8.09	6.0E-28	BE940438.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
12286	24717		1.72	6.0E-28	BF568097.1	EST_HUMAN	RC3-UT0082-210800-021-a05 UT0082 Homo sapiens cDNA
8630	21322		5.36	5.0E-28	AW887541.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
3226	15989		1.84	4.0E-28	AJ752397.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
5919	18704		7.91	4.0E-28	BE164930.1	EST_HUMAN	cnt15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnt15c02 random
7979	20874	33787	0.55	4.0E-28	AJ678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
7979	20874	33788	0.55	4.0E-28	AJ678101.1	EST_HUMAN	wd35g08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8644	21336	34480	6.21	4.0E-29	J04988.1	NT	MER29.12 MER29 repetitive element ;
4381	17118	29751	1.4	3.0E-28	AB042297.1	NT	Human 80 kD heat shock protein gene, complete cds
4684	17418	30054	1.07	3.0E-29	BF333236.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
5841	18829	31564	1.18	3.0E-29	BE314018.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
8632	21324	34466	2.87	3.0E-28	D38044.1	NT	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508627 5'
9200	21869	35034	1.69	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
9431	22109		1.87	3.0E-29	AL163246.2	NT	xv1703.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9859	22509		0.61	3.0E-28	BE350127.1	EST_HUMAN	repetitive element;contains MER19.12 MER19 repetitive element ;
11235	23898	37185	1.47	3.0E-29	AA403053.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
12102	24600		1.53	3.0E-28	D63882.1	NT	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER20.b3
12789	25376		7.53	3.0E-29	AA016177.1	EST_HUMAN	MER20 repetitive element ;
480	13265	25900	1.72	2.0E-29	AF084869.1	NT	h09g01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
							G1335769 GAG-POL POLYPYRROLINE ;
							Human HsLIM15 mRNA for HsLIM15, complete cds
							z532e09.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360712 3'
							Homo sapiens envelope protein RLC-6 (env) gene, complete cds

Page 257 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
480	13265	25901	1.72	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1523	14270	26955	6.62	2.0E-29	AI063604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1623	14270	26956	6.62	2.0E-29	AI063604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4246	16987	29610	1.63	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5735	18527	31449	0.89	2.0E-29	AI082459.1	EST_HUMAN	cs71604.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1810814 3' similar to contains L1.12 L1 repetitive element ;
6087	18865	31830	1.48	2.0E-29	AI066418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7459	18865	31830	1.36	2.0E-29	AI066418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7878	20571	33698	1.16	2.0E-29	BE067157.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
8477	21169	34313	0.63	2.0E-29	10567821	NT	601442206F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846648 5' Homo sapiens DNA-binding protein (LOC56242), mRNA
8477	21169	34314	0.63	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9408	22070	35241	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9408	22070	35242	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	35989	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	36000	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10877	23657	36804	1.31	2.0E-29	BF026947.1	EST_HUMAN	601688934F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3862833 5' Homo sapiens splicing factor similar to dnal (SPF31), mRNA
11459	24063		2.04	2.0E-29	11425108	NT	QV0-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
11499	24100		1.73	2.0E-29	AW880701.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
8691	21893	34527	7.37	1.0E-29	AW983880.1	EST_HUMAN	R.ratus RYA3 mRNA for a potential ligand-binding protein
10518	23164	36391	0.85	1.0E-29	X60658.1	NT	nz20c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
6487	19254	32255	2.97	9.0E-30	AA761215.1	EST_HUMAN	Homo sapiens zinc/ferritin regulated transporter-like (ZIRTL), mRNA
11992	24531		1.76	9.0E-30	11422745	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8227	19001		8.94	8.0E-30	F08688.1	EST_HUMAN	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
8168	20862	33994	3.72	8.0E-30	AA383873.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
8583	21275	34412	3.1	8.0E-30	AI557072.1	EST_HUMAN	PM4-BT0724-150400-004-11 BT0724 Homo sapiens cDNA
1605	14251		1.03	7.0E-30	BE091133.1	EST_HUMAN	Human mRNA for integrin alpha subunit, complete cds
1766	14508	27209	1.73	6.0E-30	D25303.1	NT	QV0-BN0147-290400-214-112 BN0147 Homo sapiens cDNA
3185	15948	28598	2.3	6.0E-30	BE008026.1	EST_HUMAN	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
10437	23063	36310	0.48	6.0E-30	AF177227.1	NT	

Page 258 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12769	17897		3.38	6.0E-30	X51766.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3994	16742	26378	26.19	5.0E-30	A1399992.1	EST_HUMAN	ig92g03.x1 NCI_CGAP_C11.1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5169	26176		6.44	5.0E-30	U87931.1	NT	Human aconitase hydratase (ACO2) gene, exon 7
10802	23485		1.95	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11103	23773	37047	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11103	23773	37048	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2139	14869	27599	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-080200-080-c06 DT0043 Homo sapiens cDNA
2139	14869	27600	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-080200-080-c06 DT0043 Homo sapiens cDNA
6766	17925	30560	0.63	4.0E-30	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8803	21495	34641	2.82	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-08 ST0181 Homo sapiens cDNA
1129	13885		2.11	3.0E-30	A1338551.1	EST_HUMAN	qq63c05.x1 Soares_tet1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1638620 3' similar to contains MER29.b2 MER29 repetitive element ;
3740	10493	29128	0.93	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
7852	20547		0.58	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8395	21078		0.48	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10333	22980	36200	1.7	3.0E-30	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
10465	23111	36342	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10465	23111	36343	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11169	23835	37116	2.48	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
660	13436	26077	0.92	2.0E-30	AW857315.1	EST_HUMAN	CM0-C10307-310100-158-h03 C10307 Homo sapiens cDNA
1062	13820		3.11	2.0E-30	F08698.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1462	14209	26896	5.31	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2720	15427	28165	8	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-176-E04 NT0101 Homo sapiens cDNA
2820	15696	28331	6.39	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3769	16521	28160	2.26	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-efo-c-12-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4727	17459	30095	1.51	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4727	17459	30096	1.51	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6660	19420	32435	0.55	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'
8375	21068	34208	0.45	2.0E-30	AA019703.1	EST_HUMAN	z68c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
8435	21126	34285	4.66	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-570C01 5'

Page 259 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8533	21225	34388	3.61	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8533	21225	34387	3.61	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8897	22547	35741	3.62	2.0E-30	AW871568.1	EST_HUMAN	EST383857 MAGC resequences, MAGL Homo sapiens cDNA P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8982	22630	35839	7.37	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876499 3' similar to contains THR.b3 THR repetitive element ;
280	13087	25729	18.33	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-570C01 5'
525	13309	25842	2.34	1.0E-30	AW468897.1	EST_HUMAN	ha30b04.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2910691 3' similar to contains MER1.B MER1 MER1 repetitive element ;
699	13474	26122	2.62	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2209	14637	27675	7.16	1.0E-30	AA664377.1	EST_HUMAN	ec7b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:868589 3'
2484	15182	27921	2.01	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157891 5'
3050	15816	28481	0.94	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7824	20290	33399	2.48	1.0E-30	BF183230.1	EST_HUMAN	601809832F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040884 5'
12581	25288		6.85	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3748	16501	29135	0.81	9.0E-31	TT3025.1	EST_HUMAN	yc55e06.r1 Stratiogene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	16501	29136	0.81	9.0E-31	TT3025.1	EST_HUMAN	yc55e06.r1 Stratiogene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8223	20917	34053	0.81	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8223	20917	34054	0.81	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30568 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8522	21214		1.63	9.0E-31	Z38283.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05103 3'
8524	21216	34359	0.48	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1054	13813	28473	2.41	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2414	15135		4.6	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4861	17590	30213	1.43	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4861	17590	30214	1.43	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
2674	15383	28123	3.29	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2674	15383	28124	3.28	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8300	20984	34130	0.96	7.0E-31	AF206541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8300	20984	34131	0.96	7.0E-31	AF206541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds

Page 260 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9168	21836		0.94	7.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12434	24805	31044	2.26	7.0E-31	X31793.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3687	16420		2.68	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8053	20747		4.37	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8229	20923	34062	0.66	6.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12169	25195		1.98	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
187	13000	25640	3.58	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
187	13000	25641	3.58	6.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8344	21037		0.73	5.0E-31	BF056540.1	EST_HUMAN	7406704.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TRQ13537 Q13537
582	13362		5.18	4.0E-31	AJ271736.1	NT	SIMILAR TO POGO ELEMENT ; contains L1.1 L1 repetitive element ;
							Homo sapiens Xq pseudautosomal region; segment 1/2
1608	14352	27040	0.91	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-LUDP
1810	14550		1.57	4.0E-31	AL163280.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
2792	15487		1.23	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
12205	24672		1.86	4.0E-31	AJ230125.1	NT	Homo sapiens chromosome 21 segment HS21C080
12457	24826		1.86	4.0E-31	11430273	NT	Homo sapiens SET domain and mafner transposase fusion gene (SETMAR) mRNA
							Homo sapiens GGT1 gene, exon 1
							Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
7239	18924	32999	12.23	3.0E-31	4829853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (18kD, ASH1) (NDUFB8) mRNA
7393	20072	33151	1.26	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8061	20755		2	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9479	22132	35312	3.7	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10408	23144	36371	0.54	3.0E-31	AA421242.1	EST_HUMAN	zu06d04.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10527	23224	36459	2.04	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11101	23771		3.65	3.0E-31	BF03527.1	EST_HUMAN	601455531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662086 5'
12819	25059		1.66	3.0E-31	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
1910	14647	27358	1.37	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-03 LT0051 Homo sapiens cDNA
2211	14939	27677	1.09	2.0E-31	AI393388.1	EST_HUMAN	tg44905.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111872 3'
2339	15052	27800	1.89	2.0E-31	AL116245.1	EST_HUMAN	DKFZp761G1513.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
							aa88f1.1.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
2442	15181	27898	4.01	2.0E-31	AA458824.1	EST_HUMAN	THR.12 THR repetitive element ;

Page 261 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5193	18001	30824	0.81	2.0E-31	AW444498.1	EST_HUMAN	UI-H-BJ3-akb-f-09-Q-J1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5824	18421	31334	3.57	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MIER29 L3
8975	21895		2.05	2.0E-31	AA877764.1	EST_HUMAN	m06f04.s1 NCI CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537
9107	21795	34959	3.64	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
9806	22457	36691	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9808	22457	35862	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
8978	22823	35828	2.35	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
8975	22823	36830	2.35	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12144	24632		1.58	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12278	25413		1.75	2.0E-31	A1114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
15	12842	25456	11.09	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1658	14404	27092	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27093	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27094	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4592	17327	29952	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
4592	17327	29953	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
5210	18018	30840	3.79	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-029-a08_1 ST0220 Homo sapiens cDNA
6042	18822	31782	2.2	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cebp1 repeat region
7189	19875	32048	1	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10138	22784	35995	0.51	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10833	23515	36757	2.7	1.0E-31	A1088434.1	EST_HUMAN	q121h03.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595
11830	24414	37752	1.48	1.0E-31	U68091.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV23S1, TCRBV10S1P, TCRBV28S1P, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY9, TRY10, TRY11, TRY12, TRY13, TRY14, TRY15, TRY16, TRY17, TRY18, TRY19, TRY20, TRY21, TRY22, TRY23, TRY24, TRY25, TRY26, TRY27, TRY28, TRY29, TRY30, TRY31, TRY32, TRY33, TRY34, TRY35, TRY36, TRY37, TRY38, TRY39, TRY40, TRY41, TRY42, TRY43, TRY44, TRY45, TRY46, TRY47, TRY48, TRY49, TRY50, TRY51, TRY52, TRY53, TRY54, TRY55, TRY56, TRY57, TRY58, TRY59, TRY60, TRY61, TRY62, TRY63, TRY64, TRY65, TRY66, TRY67, TRY68, TRY69, TRY70, TRY71, TRY72, TRY73, TRY74, TRY75, TRY76, TRY77, TRY78, TRY79, TRY80, TRY81, TRY82, TRY83, TRY84, TRY85, TRY86, TRY87, TRY88, TRY89, TRY90, TRY91, TRY92, TRY93, TRY94, TRY95, TRY96, TRY97, TRY98, TRY99, TRY100, TRY101, TRY102, TRY103, TRY104, TRY105, TRY106, TRY107, TRY108, TRY109, TRY110, TRY111, TRY112, TRY113, TRY114, TRY115, TRY116, TRY117, TRY118, TRY119, TRY120, TRY121, TRY122, TRY123, TRY124, TRY125, TRY126, TRY127, TRY128, TRY129, TRY130, TRY131, TRY132, TRY133, TRY134, TRY135, TRY136, TRY137, TRY138, TRY139, TRY140, TRY141, TRY142, TRY143, TRY144, TRY145, TRY146, TRY147, TRY148, TRY149, TRY150, TRY151, TRY152, TRY153, TRY154, TRY155, TRY156, TRY157, TRY158, TRY159, TRY160, TRY161, TRY162, TRY163, TRY164, TRY165, TRY166, TRY167, TRY168, TRY169, TRY170, TRY171, TRY172, TRY173, TRY174, TRY175, TRY176, TRY177, TRY178, TRY179, TRY180, TRY181, TRY182, TRY183, TRY184, TRY185, TRY186, TRY187, TRY188, TRY189, TRY190, TRY191, TRY192, TRY193, TRY194, TRY195, TRY196, TRY197, TRY198, TRY199, TRY200, TRY201, TRY202, TRY203, TRY204, TRY205, TRY206, TRY207, TRY208, TRY209, TRY210, TRY211, TRY212, TRY213, TRY214, TRY215, TRY216, TRY217, TRY218, TRY219, TRY220, TRY221, TRY222, TRY223, TRY224, TRY225, TRY226, TRY227, TRY228, TRY229, TRY230, TRY231, TRY232, TRY233, TRY234, TRY235, TRY236, TRY237, TRY238, TRY239, TRY240, TRY241, TRY242, TRY243, TRY244, TRY245, TRY246, TRY247, TRY248, TRY249, TRY250, TRY251, TRY252, TRY253, TRY254, TRY255, TRY256, TRY257, TRY258, TRY259, TRY260, TRY261, TRY262, TRY263, TRY264, TRY265, TRY266, TRY267, TRY268, TRY269, TRY270, TRY271, TRY272, TRY273, TRY274, TRY275, TRY276, TRY277, TRY278, TRY279, TRY280, TRY281, TRY282, TRY283, TRY284, TRY285, TRY286, TRY287, TRY288, TRY289, TRY290, TRY291, TRY292, TRY293, TRY294, TRY295, TRY296, TRY297, TRY298, TRY299, TRY300, TRY301, TRY302, TRY303, TRY304, TRY305, TRY306, TRY307, TRY308, TRY309, TRY310, TRY311, TRY312, TRY313, TRY314, TRY315, TRY316, TRY317, TRY318, TRY319, TRY320, TRY321, TRY322, TRY323, TRY324, TRY325, TRY326, TRY327, TRY328, TRY329, TRY330, TRY331, TRY332, TRY333, TRY334, TRY335, TRY336, TRY337, TRY338, TRY339, TRY340, TRY341, TRY342, TRY343, TRY344, TRY345, TRY346, TRY347, TRY348, TRY349, TRY350, TRY351, TRY352, TRY353, TRY354, TRY355, TRY356, TRY357, TRY358, TRY359, TRY360, TRY361, TRY362, TRY363, TRY364, TRY365, TRY366, TRY367, TRY368, TRY369, TRY370, TRY371, TRY372, TRY373, TRY374, TRY375, TRY376, TRY377, TRY378, TRY379, TRY380, TRY381, TRY382, TRY383, TRY384, TRY385, TRY386, TRY387, TRY388, TRY389, TRY390, TRY391, TRY392, TRY393, TRY394, TRY395, TRY396, TRY397, TRY398, TRY399, TRY400, TRY401, TRY402, TRY403, TRY404, TRY405, TRY406, TRY407, TRY408, TRY409, TRY410, TRY411, TRY412, TRY413, TRY414, TRY415, TRY416, TRY417, TRY418, TRY419, TRY420, TRY421, TRY422, TRY423, TRY424, TRY425, TRY426, TRY427, TRY428, TRY429, TRY430, TRY431, TRY432, TRY433, TRY434, TRY435, TRY436, TRY437, TRY438, TRY439, TRY440, TRY441, TRY442, TRY443, TRY444, TRY445, TRY446, TRY447, TRY448, TRY449, TRY450, TRY451, TRY452, TRY453, TRY454, TRY455, TRY456, TRY457, TRY458, TRY459, TRY460, TRY461, TRY462, TRY463, TRY464, TRY465, TRY466, TRY467, TRY468, TRY469, TRY470, TRY471, TRY472, TRY473, TRY474, TRY475, TRY476, TRY477, TRY478, TRY479, TRY480, TRY481, TRY482, TRY483, TRY484, TRY485, TRY486, TRY487, TRY488, TRY489, TRY490, TRY491, TRY492, TRY493, TRY494, TRY495, TRY496, TRY497, TRY498, TRY499, TRY500, TRY501, TRY502, TRY503, TRY504, TRY505, TRY506, TRY507, TRY508, TRY509, TRY510, TRY511, TRY512, TRY513, TRY514, TRY515, TRY516, TRY517, TRY518, TRY519, TRY520, TRY521, TRY522, TRY523, TRY524, TRY525, TRY526, TRY527, TRY528, TRY529, TRY530, TRY531, TRY532, TRY533, TRY534, TRY535, TRY536, TRY537, TRY538, TRY539, TRY540, TRY541, TRY542, TRY543, TRY544, TRY545, TRY546, TRY547, TRY548, TRY549, TRY550, TRY551, TRY552, TRY553, TRY554, TRY555, TRY556, TRY557, TRY558, TRY559, TRY560, TRY561, TRY562, TRY563, TRY564, TRY565, TRY566, TRY567, TRY568, TRY569, TRY570, TRY571, TRY572, TRY573, TRY574, TRY575, TRY576, TRY577, TRY578, TRY579, TRY580, TRY581, TRY582, TRY583, TRY584, TRY585, TRY586, TRY587, TRY588, TRY589, TRY590, TRY591, TRY592, TRY593, TRY594, TRY595, TRY596, TRY597, TRY598, TRY599, TRY600, TRY601, TRY602, TRY603, TRY604, TRY605, TRY606, TRY607, TRY608, TRY609, TRY610, TRY611, TRY612, TRY613, TRY614, TRY615, TRY616, TRY617, TRY618, TRY619, TRY620, TRY621, TRY622, TRY623, TRY624, TRY625, TRY626, TRY627, TRY628, TRY629, TRY630, TRY631, TRY632, TRY633, TRY634, TRY635, TRY636, TRY637, TRY638, TRY639, TRY640, TRY641, TRY642, TRY643, TRY644, TRY645, TRY646, TRY647, TRY648, TRY649, TRY650, TRY651, TRY652, TRY653, TRY654, TRY655, TRY656, TRY657, TRY658, TRY659, TRY660, TRY661, TRY662, TRY663, TRY664, TRY665, TRY666, TRY667, TRY668, TRY669, TRY670, TRY671, TRY672, TRY673, TRY674, TRY675, TRY676, TRY677, TRY678, TRY679, TRY680, TRY681, TRY682, TRY683, TRY684, TRY685, TRY686, TRY687, TRY688, TRY689, TRY690, TRY691, TRY692, TRY693, TRY694, TRY695, TRY696, TRY697, TRY698, TRY699, TRY700, TRY701, TRY702, TRY703, TRY704, TRY705, TRY706, TRY707, TRY708, TRY709, TRY710, TRY711, TRY712, TRY713, TRY714, TRY715, TRY716, TRY717, TRY718, TRY719, TRY720, TRY721, TRY722, TRY723, TRY724, TRY725, TRY726, TRY727, TRY728, TRY729, TRY730, TRY731, TRY732, TRY733, TRY734, TRY735, TRY736, TRY737, TRY738, TRY739, TRY740, TRY741, TRY742, TRY743, TRY744, TRY745, TRY746, 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TRY1774, TRY1775, TRY1776, TRY1777, TRY1778, TRY1779, TRY1780, TRY1781, TRY1782, TRY1783, TRY1784, TRY1785, TRY1786, TRY1787, TRY1788, TRY1789, TRY1790, TRY1791, TRY1792, TRY1793, TRY1794

Page 262 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6394	18184	30887	0.97	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-004 BN0048 Homo sapiens cDNA
4807	17638	30181	0.98	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12122	24814		8.18	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-amplified region
2735	15442	28180	1.01	8.0E-32	A1478104.1	EST_HUMAN	tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159894 3' similar to contains MER29.13
7266	19950		1.47	6.0E-32	BE888016.1	EST_HUMAN	MER29 repetitive element;
1011	13771	26431	16.78	5.0E-32	AF116627.1	EST_HUMAN	601611630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
910	13677		1.76	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
5148	17867		0.91	4.0E-32	A1985583.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7503	20174	33266	2.94	4.0E-32	11432574	NT	ws08h12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496647 3' similar to contains MER16.b3
7503	20174	33267	2.94	4.0E-32	11432574	NT	MER18 repetitive element;
8257	20951		1.2	4.0E-32	BE064410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
443	13229	25872	3.7	3.0E-32	Y17293.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1437	14184	26870	8.08	3.0E-32	AV731600.1	EST_HUMAN	RC4-BT0311-141189-011-003 BT0311 Homo sapiens cDNA
8294	21861	35135	8.38	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
8294	21861	35136	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV731600 HTF Homo sapiens cDNA clone HTFAK07 5'
10843	23525	36768	3.57	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
12146	24634		3.51	3.0E-32	BE279088.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
12507	17899	30586	2.97	3.0E-32	5174574	NT	z96a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.3 THR repetitive element;
12507	17899	30586	2.97	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12507	17899	30586	2.97	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12668	24966		2.27	3.0E-32	BE279088.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
6158	18936	31902	0.81	2.0E-32	M35418.1	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6387	19156	32156	5.32	2.0E-32	Z38133.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
8176	20870	34003	2.26	2.0E-32	AA114294.1	EST_HUMAN	H. sapiens mRNA for myosin
8176	20870	34004	2.26	2.0E-32	AA114294.1	EST_HUMAN	H. sapiens mRNA for myosin
11859	24443	37784	2.06	2.0E-32	T18882.1	EST_HUMAN	zn66c08.11 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
12763	25022	30961	2.42	2.0E-32	AV736449.1	EST_HUMAN	zn66c08.11 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
							b12056T Testis 1 Homo sapiens cDNA clone b12056
							AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'

Page 263 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12763	25022	30882	2.42	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBA08 6'
3090	16855		1.67	1.0E-32	BE743259.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6855	19437	32453	7.02	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8494	21186	34329	8.08	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.k3 THR repetitive element;
3474	16230		4.68	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6326	18096		4.05	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8887	21379	34623	1.95	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
10701	23392		5.22	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
58	12887	25517	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
58	12887	25518	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2158	14888	27622	2.29	7.0E-33	AI590115.1	EST_HUMAN	hw2b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176909 3' similar to contains OFR.t1 OFR repetitive element;
2655	15365		6.45	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3236	15998		9.3	7.0E-33	AW971307.1	EST_HUMAN	EST383386 MAGC resequences, MAGL Homo sapiens cDNA Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
8845	21537		1.56	7.0E-33	X54890.1	NT	
10732	23419	36660	2.41	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
11213	23876	37162	1.93	7.0E-33	AW971568.1	EST_HUMAN	EST383657 MAGC resequences, MAGL Homo sapiens cDNA
12127	24619	31090	4.34	7.0E-33	AA601416.1	EST_HUMAN	no16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element;
3720	16473		0.94	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5976	18758	31720	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
5976	18758	31721	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
8478	21170	34315	9.33	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8603	21295	34438	3.09	6.0E-33	11429188	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9910	22559	35755	1.12	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
9910	22559	35755	1.12	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1770	14512		1.46	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0163-100700-271-a02 FTO163 Homo sapiens cDNA
1874	14612		1.19	6.0E-33	11141894	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1891	14628	27337	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1891	14628	27338	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

Page 264 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2270	14998		1.29	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
10148	22798	36010	0.8	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752481 3'
10148	22798	36011	0.8	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752481 3'
1109	13863		2.16	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2121	14852	27581	1.84	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2419	15140		2.02	4.0E-33	AA628921.1	EST_HUMAN	ab51b11.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2547	15282	27999	4.15	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4450	17188	29811	2.15	4.0E-33	AW293349.1	EST_HUMAN	UI-H-B12-ah1-c-03-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	18122	30779	24.73	4.0E-33	AA053053.1	EST_HUMAN	z71a08.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb.X12871_rne1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6299	19072	32057	0.87	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6299	19072	32058	0.87	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1067	13825		5.5	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element ;
1068	13825		3.89	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element ;
2481	15595		0.92	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC0CF08 3'
10398	22985	35203	1.04	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Scores_festis_NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13679 Q13579 MARINER TRANSPOSASE. ;
102	12843		3.21	2.0E-33	AI160189.1	EST_HUMAN	qb87g03.x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
4385	17122		5.39	2.0E-33	BE159039.1	EST_HUMAN	MIR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
4925	17653	30285	28.91	2.0E-33	AA826883.1	EST_HUMAN	ab51g11.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb.X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5033	17753	30365	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5033	17753	30366	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5329	19099	32087	1.81	2.0E-33	AI277492.1	EST_HUMAN	q96d01.x1 Scores_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
8998	21698		2.18	2.0E-33	AI05256.1	EST_HUMAN	oz21d03.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1876973 3' similar to gb.M26536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10513	23159	36384	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10513	23159	36385	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
11046	23716	36985	1.26	2.0E-33	AA453647.1	EST_HUMAN	zx4805.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:765489 3' similar to TR:G1263081 G1263081 MARINER TRANSPOSASE. ;

Page 265 of 536  
Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8	12835		1.16	1.0E-33	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5156	17873	30485	2.48	1.0E-33	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
5501	18269	31198	0.68	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7307	19990	33087	1.04	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
9920	25432		0.84	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11292	23953	37251	1.83	1.0E-33	AW998818.1	EST_HUMAN	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
11693	24259	37581	3.32	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12407	24790		2.21	1.0E-33	A1927191.1	EST_HUMAN	w088c06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'
12570	12835		4.07	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12602	24914	31005	1.41	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
12780	25034		1.61	8.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2168	14897	27631	0.98	8.0E-34	8922761	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
7689	20353	33488	0.86	8.0E-34	BE068882.1	EST_HUMAN	MIR4-BT0399-200100-001-103 BT0399 Homo sapiens cDNA
1426	14173	26858	2.27	7.0E-34	T70845.1	EST_HUMAN	ydl15605.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
8900	14173	26858	0.56	7.0E-34	T70845.1	EST_HUMAN	ydl15605.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12191	24662		3.05	7.0E-34	H12888.1	EST_HUMAN	y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
458	13243	25884	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
458	13243	25885	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
12011	24544	31107	2.13	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hac1-) gene
1873	14611		2.9	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
5002	17725	30328	3.61	5.0E-34	U30883.1	NT	Human splicing factor SRp65-1 (SRp-55) mRNA, complete cds
8765	21457	34607	1.37	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10550	23246	36482	2.24	5.0E-34	A5037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11219	23982		1.79	6.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1991	14727	27449	1.64	4.0E-34	A1804867.1	EST_HUMAN	tt94c06.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2249194 3'
5770	18561	31488	0.64	4.0E-34	AA861773.1	EST_HUMAN	ek35c01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407938 3'
8936	21627	34769	1.26	4.0E-34	BF208778.1	EST_HUMAN	601874950FT NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4102213 5'
6138	18916	31886	0.78	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11100	23770		3.14	3.0E-34	BF03327.1	EST_HUMAN	601458531FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8850	21541	34687	1.16	2.0E-34	A1678101.1	EST_HUMAN	w035g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;

Page 266 of 536  
Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8850	21641	34698	1.18	2.0E-34	AI878101.1	EST_HUMAN	wd35g06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
11113	23783	37057	1.34	2.0E-34	P61805	SWISSPROT	MER29.12 MER29 repetitive element:
11113	23783	37058	1.34	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1494	14241	26928	6.53	1.0E-34	P12236	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
3683	18416	28055	1.32	1.0E-34	AF003526.1	NT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
4051	18786	29425	0.97	1.0E-34	AY009397.1	NT	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
4051	18786	29426	0.97	1.0E-34	AY009397.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
4448	17182	31789	3.44	1.0E-34	BE071414.1	EST_HUMAN	regions
6047	18827	31788	2.05	1.0E-34	BE074052.1	EST_HUMAN	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
6047	18827	31789	2.05	1.0E-34	BE074052.1	EST_HUMAN	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
9225	21804	36076	0.45	1.0E-34	P23266	SWISSPROT	RC2-BT0508-240400-016-108 BT0508 Homo sapiens cDNA
9566	22249	35434	7.1	1.0E-34	AL036635.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
11138	23805	37083	1.39	1.0E-34	BE781790.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
11138	23805	37084	1.39	1.0E-34	BE781790.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
11153	23820	37100	1.82	1.0E-34	11439598	NT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
12372	25350		1.65	1.0E-34	AA807097.1	EST_HUMAN	DKFZp564A1563_1 584 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564A1563 5'
12593	24949		4.22	1.0E-34	AL163210.2	NT	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
3636	16389	28029	1.2	9.0E-35	AW663302.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
218	13028		7.71	8.0E-35	6031180	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
1730	14472	27171	3.43	8.0E-35	BF589937.1	EST_HUMAN	cc31ct1.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
1730	14472	27172	3.43	8.0E-35	BF589937.1	EST_HUMAN	TYROSINE-PROTEIN KINASE RECEPTOR FL4 PRECURSOR (HUMAN);
4814	17645	30170	2.69	8.0E-35	BF183195.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
10599	23283	36522	2.42	8.0E-35	BE378480.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
12118	24611		3.95	8.0E-35	BF569282.1	EST_HUMAN	Homo sapiens prolilin (PHB) mRNA
6393	19182	32163	2.05	7.0E-35	11425417	NT	ncs33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1391	14138	26815	1.83	6.0E-35	AA767116.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
1960	14696	27409	2.08	6.0E-35	8005975	NT	ncs33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4030	16775	29408	0.84	6.0E-35	AW297191.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
							601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
							601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3008513 5'
							602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300680 3'
							Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
							ah53h03.s1 Scores_testis_NHT Homo sapiens cDNA clone 1309397 3'
							Homo sapiens zinc finger protein 208 (ZNF208), mRNA
							UH-BW0-a1d-09-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731433 3'

Page 267 of 536  
Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7798	20493	33615	3.84	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8610	21302	34446	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8610	21302	34446	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9565	22218	35403	0.96	6.0E-35	AB002394.1	NT	Human mRNA for KIAA0368 gene, partial cds
9803	22464	36656	3.17	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1704	14447	27146	1.36	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2787	15492	28232	1.07	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3008	16776	28424	1.7	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), protein1, cote1, glucocorticoidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4376	17113	28748	1.7	5.0E-35	AF023268.1	NT	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8084	20778		3.99	5.0E-35	BE890992.1	EST_HUMAN	q838c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0246.;
8109	20803	33936	2.35	5.0E-35	A1208765.1	EST_HUMAN	q838c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
8109	20803	33937	2.35	5.0E-35	A1208765.1	EST_HUMAN	q838c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
11130	23788		2.46	5.0E-35	AA001786.1	EST_HUMAN	z184f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428016 5'
1413	14161	26846	16.86	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
							y99a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;
1811	14551	27265	4.87	4.0E-35	H91193.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4753	17485		0.72	4.0E-35	AF003528.1	NT	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
7108	19706		1.81	4.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element;
8416	21109	34248	8.89	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434L148 5'
11729	24322	37646	1.38	4.0E-35	AW303317.1	EST_HUMAN	xx17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
1573	14320	27008	7.76	3.0E-35	BE288182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2330	15055		1.5	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
							7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:35655361 3' similar to TR:Q9QZH7
5268	18062	30680	31.47	3.0E-35	BF433100.1	EST_HUMAN	Q9QZH7 F-BOX PROTEIN FBL2.;
5268	18062	30691	31.47	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:35655361 3' similar to TR:Q9QZH7
							Q9QZH7 F-BOX PROTEIN FBL2.;

Page 268 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9388	22060		1.42	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10074	22722	35939	1.12	3.0E-35	AW003063.1	EST_HUMAN	wr03a05.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10286 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
106	15535	25587	1.88	2.0E-35	N88965.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
1165	13919	26592	1.55	2.0E-35	T11909.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
2215	14943	27683	5.73	2.0E-35	AB018413.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0671), mRNA
3306	16066	28714	1.12	2.0E-35	9912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3306	16066	28715	1.12	2.0E-35	9912459	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3545	16300		0.84	2.0E-35	AB020702.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16640	29279	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16840	29280	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4821	17356		2.57	2.0E-35	H49239.1	EST_HUMAN	Yq19a12.1f Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 6'
5495	18294	31192	2.7	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-004 BT0701 Homo sapiens cDNA
7004	19688	32749	0.95	2.0E-35	BE832636.1	EST_HUMAN	GM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7004	19696	32750	0.95	2.0E-35	BE832636.1	EST_HUMAN	GM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7776	20471	33593	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAY10 5'
7775	20471	33594	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAY10 5'
10697	23388	36626	2.24	2.0E-35	X99417.1	NT	H. sapiens PROS-27 mRNA
11817	18294	31192	1.28	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-004 BT0701 Homo sapiens cDNA
11889	16066	28714	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11889	16066	28715	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12062	24577	31120	1.36	2.0E-35	BE904978.1	EST_HUMAN	G01496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12062	24577	31121	1.36	2.0E-35	BE904978.1	EST_HUMAN	G01496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12372	24900		5.98	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12689	15535	25567	1.56	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
45	12874	25496	6.81	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	12874	25497	6.81	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	13509	28166	19.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-S10162-131099-008-d12 S10162 Homo sapiens cDNA

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736	13608	26166	19.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0182-131098-008-d12 ST0182 Homo sapiens cDNA
889	13658		1.3	1.0E-35	T87947.1	EST_HUMAN	y493a01.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2644	15268	27986	1.88	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2770	15475	28217	1.09	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3
2770	15475	28217	1.09	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element ;
2770	15475	28218	1.09	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element ;
3140	15804	28549	1.81	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCBE1L) mRNA
3161	15924	28570	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCOEF08 3'
3161	15924	28571	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCOEF08 3'
4388	17125	29766	3.93	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4388	17125	29767	3.93	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5423	18222	30934	1.41	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7363	20063	33141	0.88	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7641	20211	33311	1.18	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9442	25125	35297	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACES3 Homo sapiens cDNA clone PLACE3000382 3'
9442	25125	35298	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACES3 Homo sapiens cDNA clone PLACE3000382 3'
10477	23123	36352	0.7	1.0E-35	BF589594.1	EST_HUMAN	nea06d08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10477	23123	36353	0.7	1.0E-35	BF589594.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ;
11758	24349	37680	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11758	24349	37681	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11758	24359		1.91	1.0E-35	AI525119.1	EST_HUMAN	promme-7.D01.r b1rutor Homo sapiens cDNA 5'
11817	26313		1.37	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12121	24613		1.63	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12471	24837		2.13	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
9129	21817	34983	0.58	8.0E-36	AA348480.1	EST_HUMAN	EST54698 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2831	15897	28344	1.1	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
3116	15881		3.84	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7554	20224	33327	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
7554	20224	33328	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN

Page 270 of 536  
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Single Exon Probes Expressed In Brain

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1698	14794	27466	2	6.0E-36	7706822	NT	Homo sapiens nitrofurin 2 (NINJ2), mRNA
2418	15139		6.58	6.0E-36	AB035346.1	NT	Homo sapiens TOLB gene, exon 12
3630	16383	28023	0.71	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-amy-c-12-0-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5248	18054	30692	3.54	6.0E-36	A1495169.1	EST_HUMAN	ih93p08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126196 3' similar to
							gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
							h06h02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMAZ_HUMAN
							P62292 IMPORTIN ALPHA-2 SUBUNIT ;
7009	19701	32756	3.57	6.0E-36	AW780143.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
8650	21242	34385	2.33	6.0E-36	AF208161.1	NT	C16927 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-535C11 5'
10125	22773		0.51	6.0E-36	C16927.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
11538	24138	37443	3.11	6.0E-36	A1380499.1	EST_HUMAN	h05609.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MIER9.b2
134	12949	26592	10.74	6.0E-36	AJ271735.1	NT	MER9 repetitive element ;
2755	15460	28202	5.76	6.0E-36	BE388436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
3589	16352	28901	1.45	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607288 5'
4738	17468	30104	2.15	6.0E-36	5728729	NT	Homo sapiens chromosome 21 segment HS21C009
4738	17468	30104	2.15	6.0E-36	5728729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
4738	17468	30105	2.15	6.0E-36	5728729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
7686	20350	33464	0.61	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
11897	12949	26592	3.63	6.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12188	24650	31103	3.45	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1203	13955	26819	1.69	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100-00-001-g04 BN0176 Homo sapiens cDNA
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1423	14170	26856	1.03	4.0E-36	P10266	SWISSPROT	ENDONUCLEASE
1640	14386	27074	1.61	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3628386 5'
2219	14947		2.13	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3349	16108	28763	0.82	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3349	16108	28764	0.82	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5629	18425		0.84	4.0E-36	R64023.1	EST_HUMAN	yl1805.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:139713 5'
5954	18746	31707	2.33	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7553	20223	33326	1.63	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIB (GPIIb) gene, exons 2-29
8453	21145	34285	1.62	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8453	21145	34286	1.62	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10909	23599	36835	2.84	4.0E-36	AA400370.1	EST_HUMAN	zu69c10.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743250 5'
12183	24655		2.09	4.0E-36	11420518	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFA1C2), mRNA
12227	25199		7.3	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TFGABH01 5'

Page 271 of 536  
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Single Exon Probes Expressed in Brain

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12798	26047		1.44	4.0E-36	D5217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
680	13455	28100	2.58	3.0E-36	AF09810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
1484	14231	28917	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1484	14231	26918	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2287	15022	27757	1.21	3.0E-36	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4487	17203	28828	6.88	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
11050	23720	30891	1.59	3.0E-36	BF035327.1	EST_HUMAN	60146853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3187	16830	28579	2.38	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
4904	17631	30248	6.45	2.0E-36	AW880378.1	EST_HUMAN	QV0-O10030-240300-174-h04 O10030 Homo sapiens cDNA
5398	18198	30882	3.1	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
6758	18550	31471	3.95	2.0E-36	T08756.1	EST_HUMAN	EST006648 Infant Brain, Benho Scores Homo sapiens cDNA clone HIBB128 5' end
6481	19248	32248	12.22	2.0E-36	T68629.1	EST_HUMAN	yc44407.1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9288	21955	35126	1.07	2.0E-36	BF512784.1	EST_HUMAN	UI-H-BW1-arnu-a-T1-Q-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9449	21999	35172	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
8449	21999	35173	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
865	13634	26304	1.81	1.0E-36	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2141	14871	27603	1	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA
2199	14928	27604	1	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA
3339	16099		1.36	1.0E-36	BF673761.1	EST_HUMAN	602136463F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
5810	18599	31627	1.16	1.0E-36	AF158962.1	NT	Homo sapiens human endogenous retrovirus W, protease (pro) gene, partial cds
6090	18868		1.28	1.0E-36	4827084	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6296	19098	32052	4.19	1.0E-36	AI887714.1	EST_HUMAN	w537c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307882 3' similar to contains Alu repetitive element
6286	19099	32053	1.21	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6582	19345	32359	0.73	1.0E-36	AL120542.1	EST_HUMAN	yg36g10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
7326	20099	33087	0.85	1.0E-36	11426108	NT	DKFZp761A229_r1 761 (synonym: harny2) Homo sapiens cDNA clone DKFZp761A229 5'
7326	20099	33088	0.85	1.0E-36	11426108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAMT1), mRNA
7860	20555	33679	5.13	1.0E-36	AA148034.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAMT1), mRNA
7860	20555	33680	5.13	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
							zo51a12.r1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'

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7952	20647	33770	1.34	1.0E-36	AA420467.1	EST_HUMAN	nc60608.1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
7952	20647	33771	1.34	1.0E-36	AA420467.1	EST_HUMAN	nc60608.1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745670
8079	20773	33902	0.61	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8079	20773	33903	0.61	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8927	21618	34762	2.71	1.0E-36	AW103658.1	EST_HUMAN	xs82b07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614357 3'
10014	22662	35878	3.88	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
10226	22874	36086	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 GT0279 Homo sapiens cDNA
10226	22874	36087	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 GT0279 Homo sapiens cDNA
10867	23547	36795	3.3	1.0E-36	AW855868.1	EST_HUMAN	OM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11854	24044	37347	4.17	1.0E-36	AW504143.1	EST_HUMAN	UHF-BN0-ale-c-03-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
11393	23959	37302	1.45	1.0E-36	A905536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo sapiens cDNA
11393	23959	37303	1.45	1.0E-36	A905536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo sapiens cDNA
12060	24676		3.81	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12501	24655		3.03	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12747	25011		3.23	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7281	19965	33042	2.12	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7281	19965	33043	2.12	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12309	24733		1.35	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
3350	16109	28765	0.99	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5168	17977		1.58	8.0E-37	BE698077.1	EST_HUMAN	GM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5738	18530	31451	3.75	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5738	18530	31452	3.75	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5787	18578	31507	8.24	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element ;
7784	20479	33604	6.22	8.0E-37	X87344.1	NT	MER29 repetitive element ;
1262	14011		3.03	7.0E-37	AL042800.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1738	14480	27179	0.97	7.0E-37	AF111167.2	NT	H.sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1738	14480	27180	0.97	7.0E-37	AF111167.2	NT	DKFZp434E0422_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434E0422 5'
10657	23348	36585	8.69	7.0E-37	A817700.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							wk25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
							PTR5 repetitive element ;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10811	23494	38729	2.25	7.0E-37	AI535702.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element
8338	21031	34168	1.34	6.0E-37	AF169889.1	NT	Homo sapiens proteoglycan alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12624	24929		2.94	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6002	18783	31744	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6002	18783	31745	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8654	21346	34480	0.9	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCBHG09 5'
10837	23519		4	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12055	24572		6.86	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2423	15144	27877	2.12	4.0E-37	AA702794.1	EST_HUMAN	280604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6184	18970	31945	0.81	4.0E-37	AW794502.1	EST_HUMAN	RC6-JM0014-210200-021-H05 UM0014 Homo sapiens cDNA
8266	21935	35109	0.74	4.0E-37	AA843808.1	EST_HUMAN	ak09c02.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2010	14745	27472	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2010	14745	27473	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2965	15731		3.15	3.0E-37	AW981150.1	EST_HUMAN	EST737222 MAGe resequences, MAGe Homo sapiens cDNA
6774	18565	31494	0.92	3.0E-37	AL138274.1	EST_HUMAN	DKFZp47G067_r1 547 (synonym: hfer1) Homo sapiens cDNA clone DKFZp47G067 5'
7456	20129	33221	0.71	3.0E-37	AI748952.1	EST_HUMAN	al34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373899 3' similar to TR:Q13537
372	13197	25842	0.68	2.0E-37	D89790.1	NT	Q13537 SIMILAR TO POGO ELEMENT. ; Homo sapiens mRNA for AML1, complete cds
372	13197	25843	0.68	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1058	13816	28477	2.64	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1058	13816	28478	2.64	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1956	14882	27405	1.97	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3873	16023	29261	4.78	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4988	17693		0.93	2.0E-37	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5304	18109		0.66	2.0E-37	BF035327.1	EST_HUMAN	60145853F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
6561	19326	32333	3.46	2.0E-37	AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
7895	20590	33720	0.46	2.0E-37	BE537794.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
7895	20590	33721	0.46	2.0E-37	BE537794.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
7937	20632	33759	2.88	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11549	24148	37459	11.22	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12784	25037		3.54	2.0E-37	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2081	14813	27546	4.93	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Page 274 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3192	16955		1.08	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3943	16993	29332	0.72	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4888	17615	30234	2.35	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
5914	18699		0.94	1.0E-37	7305360	NT	Mus musculus otogelin (Otog), mRNA
8113	20807	33940	1.25	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8634	21928	34468	2.57	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:3458308 5'
10597	23291	36528	2.96	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12363	24768		2.81	1.0E-37	BE771814.1	EST_HUMAN	OM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
5690	18483	31402	2	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC68768), mRNA
1200	13952	26916	2.02	8.0E-38	11436955	NT	Homo sapiens Gb2-associated binder 2 (KIA00571), mRNA
2502	15219	27962	1.8	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153992 5'
12420	13952	26616	1.6	8.0E-38	11436955	NT	Homo sapiens Gb2-associated binder 2 (KIA00571), mRNA
4197	16938	28563	0.73	7.0E-38	H19092.1	EST_HUMAN	yp5107.r1 Soares adult brain N2b5H-B55Y Homo sapiens cDNA clone IMAGE:171973 5'
5039	17758		1.31	7.0E-38	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
3037	15903	28450	1.2	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3869348 5'
5502	18300	31189	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5502	18300	31200	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7228	19913	32986	0.57	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
11918	24480		2.67	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12395	24783	31038	12.79	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12767	25161	30900	1.7	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
710	13484	26133	1.38	5.0E-38	AW971818.1	EST_HUMAN	EST383808 IMAGE resequences, MAGL Homo sapiens cDNA
2455	15173	27912	0.99	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
3849	16446	29086	0.85	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3917	16667	29307	0.92	5.0E-38	T63107.1	EST_HUMAN	y440h07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:110749 5' similar to SP-OLF3_MOUSE P23275 OLFACTORY RECEPTOR ;
3917	16667	29308	0.92	5.0E-38	T63107.1	EST_HUMAN	y440h07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:110749 5' similar to SP-OLF3_MOUSE P23275 OLFACTORY RECEPTOR ;
6930	19666	32712	1.48	5.0E-38	BE971610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3864074 5'
116	12936	25575	4.59	4.0E-38	Z25496.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
116	12936	25576	4.59	4.0E-38	Z25496.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2093	14824		5.25	3.0E-38	AF003630.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3684	16437		2.19	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA

Page 275 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3836	16587	29224	1.76	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3836	16587	29225	1.76	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4574	17309		1.47	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6555	25097	32430	8.11	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7144	19831	32900	0.56	3.0E-38	AW302461.1	EST_HUMAN	xx04401.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2827009 3'
7488	20160	33252	8.26	3.0E-38	BF373694.1	EST_HUMAN	CM3-F10181-140700-241-f07 F10181 Homo sapiens cDNA
8548	21240	34383	2.1	3.0E-38	H85494.1	EST_HUMAN	yw8b04.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
8548	21240	34384	2.1	3.0E-38	H85494.1	EST_HUMAN	yw8b04.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
9872	22522		2.24	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12630	17896	30488	1.65	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
49	12878	25504	1.4	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	14106	28781	2.89	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1841	14387	27076	2.21	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1841	14387	27076	2.21	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2408	15129	27885	1.45	2.0E-38	W76571.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
5632	18427	31339	0.69	2.0E-38	Z26834.2	NT	z068g09.r1 Soares_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:345694 5'
5632	18427	31340	0.69	2.0E-38	Z26834.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7619	20285	33385	1.46	2.0E-38	AV721103.1	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
8382	21075		4.38	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8793	21485	34631	0.56	2.0E-38	F08450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8864	21555	34700	2.04	2.0E-38	AF069765.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
							Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9121	21809		1.06	2.0E-38	BE222258.1	EST_HUMAN	hu08g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPROTEIN ;
10346	22993	36212	1.71	2.0E-38	D83479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11200	23865	37151	1.37	2.0E-38	AA595480.1	EST_HUMAN	no34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11200	23865	37152	1.37	2.0E-38	AA595480.1	EST_HUMAN	no34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
11472	24073	37392	5.79	2.0E-38	BE172790.1	EST_HUMAN	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
11638	24236	37557	3.52	2.0E-38	AF180501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds

Page 276 of 536  
Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	24236	37668	3.52	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11971	24517		3.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHD7 5'
11973	24518		2.08	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12260	24705	31081	6.45	2.0E-38	H55841.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12323	24742		1.43	2.0E-38	S74806.1	NT	E1 beta=pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt]
12777	25031		3.76	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1071	13829		2.55	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742339 5' similar to contains element
1992	14728	27450	2.53	1.0E-38	4885288	NT	MER19 repetitive element
2012	14747	27475	1.11	1.0E-38	7681969	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2499	15216	27960	2.34	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4280	17029	29655	1.23	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4290	17029	29655	1.23	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4558	17293	29921	1	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
5937	18719	31677	4.71	1.0E-38	7305360	NT	Mus musculus obogelin (Otog), mRNA
5937	18719	31678	4.71	1.0E-38	7305360	NT	Mus musculus obogelin (Otog), mRNA
7304	19987	33063	3.16	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9051	21740	34898	0.71	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
9310	21977	36160	5.13	1.0E-38	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10301	22948	36163	0.68	1.0E-38	R18512.1	EST_HUMAN	MER29 repetitive element
11588	24187	37503	1.28	1.0E-38	7682109	NT	yf86b08.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:30486 5'
12118	25140		2.2	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
53	12882	25510	15.3	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1373	14121	26796	1.45	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1821	14560		1.27	8.0E-39	AI823404.1	EST_HUMAN	wh33f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384461 3' similar to TR:P87880 P87880
2087	14819	27650	5.79	7.0E-39	AL163227.2	NT	POL PROTEIN
10711	23400	36639	2.24	6.0E-39	BF331829.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
12896	24979		1.68	6.0E-39	BE970394.1	EST_HUMAN	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
987	13760	26412	1.57	5.0E-39	AF003528.1	NT	7e34c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R161.6
							CE00828
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2984	15760	28397	8.62	5.0E-39	A1750154.1	EST_HUMAN	at3604.x1 Barelead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q16408
12410	24793		2.04	5.0E-39	11420289	NT	Q16408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.11 LTR7 repetitive element ;
637	13320	25954	6.78	4.0E-39	AB016610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3559	16314	28961	0.97	4.0E-39	AL163210.2	NT	Chlorocebus ethiops mRNA for ribosomal protein S4X, complete cds
7974	20669	33791	1.27	4.0E-39	AA082949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	ae92g04.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9228	21907	35079	0.56	4.0E-39	D84116.1	NT	OFB.b1 OFR repetitive element ;
12427	24802		4.47	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12534	24878		2.71	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
46	12876	25498	14.86	3.0E-39	AA631949.1	EST_HUMAN	QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
46	12875	25499	14.88	3.0E-39	AA631949.1	EST_HUMAN	fnf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25500	14.86	3.0E-39	AA631949.1	EST_HUMAN	fnf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11983	24511	37257	4.35	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
11983	24511	37258	4.35	3.0E-39	A1084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12006	24541		6.82	3.0E-39	H37803.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
877	13846		6.8	2.0E-39	BE408203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
882	13681		14.08	2.0E-39	A1525119.1	EST_HUMAN	yp51c08.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:190954 3'
1009	13769		4.2	2.0E-39	AF000573.1	NT	607301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638289 5'
1520	14287		11.91	2.0E-39	AW372318.1	EST_HUMAN	promme-7 D01.r bvtumor Homo sapiens cDNA 5'
1966	14702	27419	3.28	2.0E-39	AA720574.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
2634	16346	28089	1.84	2.0E-39	AL163248.2	NT	PM0-BT0340-211289-003-002 BT0340 Homo sapiens cDNA
4370	17108	28743	1.48	2.0E-39	BF370207.1	EST_HUMAN	mw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
5403	18203	30907	4.21	2.0E-39	AA808880.1	EST_HUMAN	THR repetitive element ;
7269	18953	33029	2.36	2.0E-39	AA080867.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7431	20108	33185	0.72	2.0E-39	AL163202.2	NT	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
7431	20108	33196	0.72	2.0E-39	AL163202.2	NT	ng65f03.s1 NCL_CGAP_P18 Homo sapiens cDNA clone IMAGE:941683
8209	20803	34038	0.67	2.0E-39	AF078779.1	NT	zn06f02.r1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
9394	22060		0.55	2.0E-39	AA984631.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
							Homo sapiens chromosome 21 segment HS21C002
							Rattus norvegicus putative four repeat tcn channel mRNA, complete cds
							am88c11.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630186 3'

Page 278 of 536  
Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9826	22179		0.73	2.0E-39	AI886960.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253082 3'
11409	24058	37365	2.97	2.0E-39	D86964.1	NT	Human mRNA for KIAA0208 gene, partial cds
1503	14249	28938	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1503	14249	26937	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1521	14268	26952	4.24	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4098	16841	29467	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4098	16841	29468	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4612	17347	29980	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364085 MAGI2 resequences, MAGB Homo sapiens cDNA
4612	17347	29981	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364085 MAGI2 resequences, MAGB Homo sapiens cDNA
4654	17388	30021	8.86	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5274	18079	30736	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5274	18079	30736	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5542	18339	31246	1.97	1.0E-39	T80876.1	EST_HUMAN	yt28g06.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element; contains LTR1 repetitive element ;
5578	18375	31287	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
5578	18375	31288	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
6727	18561		1.57	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7264	19948	33025	1.8	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8462	21154	34297	1.03	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNAse K6)
12357	24761		1.34	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
542	13326	25957	1.88	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphatase 2 (UGP2), mRNA
1213	13963	26629	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1213	13963	26630	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1432	14179	26865	6.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3766	16517	29156	0.97	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3958	17878	28343	3.98	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3036	19502	28449	0.84	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H15A04
3903	16653		3.35	8.0E-40	BE306541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 5'
7616	20282	33390	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds

Page 279 of 536  
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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7616	20282	33391	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10813	23496	36732	2.27	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2730	15437	28174	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2730	15437	28175	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5849	18636		2.24	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3210480 3'
6056	18635		1.11	6.0E-40	7661899	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
6836	19498	32522	3.56	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6836	19498	32523	3.56	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9877	22627	35722	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
9877	22627	35723	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
1869	14607	27318	1.78	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN ;
2101	14832		2.27	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4356	17094	29729	9.08	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7786	20481	33606	0.5	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
7890	20585	33714	6.22	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.r1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8953	21644	34793	6.17	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-H12 BN0167 Homo sapiens cDNA
8953	21644	34794	5.17	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-H12 BN0167 Homo sapiens cDNA
10616	23309	36548	3.03	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4111	16854	29481	1.02	3.0E-40	AI925949.1	EST_HUMAN	wh12f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6543	19308	32313	7.02	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8280	20974	34116	3.62	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8898	21559	34704	1.25	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9111	21789	34963	1.42	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11232	23895	37182	8.36	3.0E-40	6005613	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
11563	24162	37473	2.23	3.0E-40	AW118799.1	EST_HUMAN	xd86h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERV'S ;
317	13120		8.63	2.0E-40	AI223036.1	EST_HUMAN	gg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
777	13649		1.61	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781088 3' similar to SW:RS5_MOUSE
1818	14957		0.92	2.0E-40	AV731801.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6 ;
1927	14663	27376	1.58	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1927	14663	27376	1.58	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2084	14796	27522	1.21	2.0E-40	AI068562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2166	14895	27630	2.48	2.0E-40	5453592	NT	w90a11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2895	15404		1.44	2.0E-40	BE275932.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3123	15888	28529	4.28	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
4843	17573	30197	1.88	2.0E-40	AL163280.2	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4843	17573	30198	1.68	2.0E-40	AL163280.2	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
863	13632		1.78	1.0E-40	AA225899.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2827	15339	28083	0.93	1.0E-40	BF036881.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2692	15401		1.34	1.0E-40	BE018348.1	EST_HUMAN	nc09a09.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2741	15447	28185	1.18	1.0E-40	BF541030.1	EST_HUMAN	601460376F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
2741	15447	28186	1.18	1.0E-40	BF541030.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
3292	16053		1.27	1.0E-40	4507142	NT	SYNTAXIN 17 ;
4571	17308	29934	4.52	1.0E-40	4508012	NT	602088604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
6161	18938	31907	0.75	1.0E-40	W92708.1	EST_HUMAN	602088604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
6161	18938	31908	0.75	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens sorting nexin 3 (SNX3) mRNA
6987	19880	32727	1.77	1.0E-40	AA573201.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6987	19880	32728	1.77	1.0E-40	AA573201.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7133	19820	32886	0.69	1.0E-40	P26808	SWISSPROT	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
10834	23516	36768	8.34	1.0E-40	AU148345.1	EST_HUMAN	n42804.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
11694	24289	37612	1.89	1.0E-40	AA614255.1	EST_HUMAN	n42804.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
11694	24289	37613	1.89	1.0E-40	AA614255.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
12376	25274		10.09	1.0E-40	BF334112.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
7822	20517	33643	1.62	8.0E-41	AL163203.2	NT	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
							np08h03.s1 NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1116861 similar to TR:G1138408
							G1138408 KIAA0173 PROTEIN ;
							np08h03.s1 NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1138408
							G1138408 KIAA0173 PROTEIN ;
							MR2-GT0222-211095-002-210 CT0222 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C003